

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Janet Epps-Ford Location: rem/2c05/2c18

Art Unit: 1635

Wednesday, July 13, 2005

Case Serial Number: 09/753169

From: Mary Jane Ruhl

Location: Biotech-Chem Library

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Epps-Ford,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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sw model - nucleic search, using OM nucleic

4, 2005, 15:50:53; Search time 258.033 Seconds (without alignments) 406.880 Million cell updates/sec February Run on:

US-09-753-169A-1 20 Title: Perfect score:

1 ctcaaccagtccattgtcca 20 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4134886 seqs, 2624710521 residues

Searched:

8269772 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed 0B 0B Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04:* : geneseqn1980s:* geneseqn1990s:* Database :

geneseqn2003ds: geneseqn2003as:* geneseqn2001as:* geneseqn2002bs:* geneseqn2001bs: geneseqn2003cs geneseqn2000s:* geneseqn2003bs: geneseqn2002as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

	•	Description		Aaz46971 BC1-X1 mR	Ach73889 Human gen	Aag81699 Human thy	Abz83507 Toxicolog	Adi32132 Human CDN	Adh52632 Chinese h	Aag81698 Human thy	Aat40079 Bcl-XL ge	Aaz93614 Bcl-x gen	Aas15189 Human bcl	Aac90810 Human Bcl	Abk84766 Human cDN	Abt16641 Human bcl	Add56779 Human bcl	Aad64187 Human bcl	Adi32104 Human cDN	Adh52630 Human ant	Ado19990 Human PRO	Adpl3351 Renal cel	Aav17638 Mouse BCL	Ade85177 Farnesyl
SUMMARIES		ID		AAZ46971	ACH73889	AAQ81699	ABZ83507	ADI32132	ADH52632	AAQ81698	AAT40079	AAZ93614	AAS15189	AAC90810	ABK84766	ABT16641	ADDS6779	AAD64187	ADI32104	ADH52630	ADO19990	ADP13351	AAV17638	ADE85177
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AAF75960 ADB58615 ADB53263 ADB53263 ADB59403 ADN04260 ADD10717 ADB10717 ABK99834 ABK99833
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ALIGNMENTS

Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Bcl-Xl mRNA specific antisense oligo A. AAZ46971 standard; DNA; 20 BP (first entry) WO200001393-A2. 14-APR-2000 Homo sapiens 13-JAN-2000. AAZ46971;

99WO-US015250. 02-JUL-1999;

98US-00109614. 02-JUL-1998;

(UYCO) UNIV COLUMBIA NEW YORK.

Stein CA;

WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bel-xL, useful for reducing bel-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English

which reduce or eliminate expression of the anti-apoptotic protein bellat. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of boll-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular The invention provides antisense oligonucleotides or their derivatives

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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-Xl mRNA
                                                                                                                                                                                                                                                                                           Gaps
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alternative splicing event; genomic alteration.
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US2003194704-A1

16-OCT-2003

03-APR-2002; 2002US-00029386

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK

WPI; 2004-119264/12

human New human genome-derived single exon nucleic acid probes useful for huma gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 15; SEQ ID NO 7084; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid soft any of the above- mentioned amino acid soft sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing

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This DNA may be expressed recombinantly for the production of a BCL-

Claim 5; Page 98; 127pp; English.

cancers.

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human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying crissues to detect the probes are used in identifying and characterising in addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising substractions in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human called form part of the primited specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL-XS; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis; multiple sclerosis; ss.
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ID AAQ81699 standard; DNA; 737
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The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also determining the presence of a toxic response to the agent. Also determining the presence of a toxic response to the agent. Also cash the service of a toxic response penes corresponding to the partial sequences given in ABZ82842 to ABZ84764, or their fragments of at least 20 nucleotides, or homologues cresponse gene plays a role on toxic response pathways by determining the espension profile of the gene after exposine of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) expositing cells to an agent or isolating cells from a human subject who was exposed to an agent or isolating the test gene expression profile for a putetively identified toxic response gene after exposure to a known coxic pharmaceutical or industrial agent; and (c) comparing the test comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of the methods are useful for
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protein, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis. (Updated on 25-MAR -2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of
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                                                                                                                                                                                                 Pred. No. 5.1;
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The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic conditions to form one or more hybridisation complexes, detecting the nucleic conditions to form one or more hybridisation complexes and comparing the levels of the detected hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes orderelates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the diagnosis of an immunopathology, such as Crohn's disease, asthma, clearive colitis, hypereoinophilia, irritable bowel syndrome, osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.
                    or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals
predicting and determining toxicological responses on a cellular, organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, gene, ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiathmatic; antiulcer;
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                                                                                                               100.0%; Score 20; DB 10; Length 737; 100.0%; Pred. No. 5.1;
                                                                          Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;
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nes 20; Conserv
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51 CTCAACCAGTCCATTGTCCA 32

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AAQ81698 standard; DNA; 926

AAQ81698/c

RESULT

(first entry)

(revised)

25-MAR-2003 10-AUG-1995

AAQ81698;

Human thymus BCL-XL DNA.

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identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genetically engineered hamster or murine myeloma host cells comprising enhanced levels of active anti-apoptosis genes, useful for producing complex protein therapeutics.
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                                                                                                                                                                                                  100.0%; Score 20; DB 11; Length 737; 100.0%; Pred. No. 5.1; cive 0; Mismatches 0; Indels (
                                                                                                                                                                 Sequence 737 BP; 181 A; 209 C; 198 G; 149 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 863 BP; 212 A; 227 C; 247 G; 177 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chinese hamster anti-apoptosis bcl-xL wild-type DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOEH ) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
                                                                                                                                 from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fussenegger M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 57; SEQ ID NO 3; 46pp; English.
                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2003; 2003US-00402017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-APR-2002; 2002US-0369307P
                                                                                                                                                                                                                                                                                                                                                                                                          ADH52632 standard; DNA; 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enenkel B, Meents H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-033642/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cricetulus griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ADH52633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003219871-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH52632;
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and
                                                                                                       BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis; multiple sclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 94; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 CTCAACCAGTCCATTGTCCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTCAACCAGTCCATTGTCCA 20
                                                                                                                                                                                                                                                                                                                                                                                           Nunez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT40079 standard; cDNA; 926
                                                                                                                                                                                                                                                                                               94WO-US007089
                                                                                                                                                                                                                                                                                                                         93US-00081448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                         Boise LH,
                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                 (ARCH-) ARCH DEV CORP
(UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-052079/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR68887
                                                                                                                                                                                                                                                                                                                                                                                         Thompson CB,
                                                                                                                                                                                                                                             WO9500642-A1
                                                                                                                                                                                                                                                                                               22-JUN-1994;
                                                                                                                                                                                                                                                                                                                         22-JUN-1993;
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                       05-JAN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT40079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancers
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ID AAT400'
XX
AC AAT400'
XX
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Local Similarity 100.

Ies 20; Conservative

Query Match

Matches

1 CTCAACCAGTCCATTGTCCA 20

100.0%; Score 20; DB 12; Length 863; 100.0%; Pred. No. 5.2;

Homo

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Antisense inhibition of bcl-x and bcl-xs expression results in apoptosis. Antisense oligonucleotides directed against bcl-x alter the ratio of bcl-x is foromas expressed by a cell or tissue (i.e. increases or decreases the ratio of bcl-xl to bcl-xs expressed) by altering the splicing of the RNA encoding bcl-x. The antisense oligonucleotide is specifically targeted to a transcript comprising two splice sites which when contacted with the transcript, reduces the relative frequency of splicing at the second splice site so that the resulting ratio of RNA splice products is altered. The use of antisense compounds sensitises cells to the effects of apoptotic stimulants such as a cellular signaling molecule, ultraviolet radiation, a cancer chemotherapeutic drug (e.g. VP-16, cisplatinum or taxol), ceramide (e.g. staurosporine) or a cytokine which causes mitochondrial dysfunction (especially loss of mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function). The antisense oligonucleotides may have a therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense oligonucleotides targeted to, and capable of inhibiting the expression of, bcl-x nucleic acids, useful for sensitizing cancer cells
                                                                                    Bcl-x; bcl-xs; antisense; therapy; apoptosis; splice site;
cell signalling molecule; ultraviolet radiation; UV; cancer;
chemotherapy; cytokine; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 3; Length 926; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dean NM, Monia BP, Nickoloff BJ,
                                                                                                                                                                                                                                                                                     /product= "Bcl-x polypeptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 102-103; 115pp; English.
                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          role in the treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00167921.
                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US022448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00277020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00323743
    (first entry)
                                                                                                                                                                                                                                                .836
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to apoptotic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-303730/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY83223
                                                                                                                                                                                                                                                                                                                                  WO200020432-A1
    16-AUG-2000
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                              13-APR-2000
                                               Bcl-x gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
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                                                                                                                                                                                                                       Key
    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes human bcl-XL protein, which protects T-lymphocytes against cell death. The genomic bcl-X gene may produce 2 different mRNAB, one encoding a long form (bcl-XL), the other a short form (bcl-XS), can encoding a long form (bcl-XL), the other a short form (bcl-XS), can be a short form bcl-XB.

Coding exon to a more proximal 5'-splice donor within the lst coding coding exon to a more proximal 5'-splice donor within the lst coding coding exon to a more proximal 5'-splice donor within the lst coding coding exon to a more proximal 5'-splice donor within the lst coding coding exon to use the bcl-XL conversion. The gene may be confinible interaction with antagonistic Bad protein, by modification of the Bcl-X homology domains BHI and/or BHZ. The bcl-XL gene may be introduced into T-cells in vivo or ex vivo via gene transfer using a vector for HIV infection gene therapy, to augment intracellular bcl-XL protein levels and protect from cell death. A corresponding antisense oligonucleotide or expression vector may be used in gene therapy of e.g. autoimmune disease, graft rejection or graft-versus-host disease, to induce cell death (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing or preventing death of T cells by bcl-XL protein regulation used to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-lymphocyte
                                                                                 Human, bcl-XL, T-lymphocyte; cell death; gene therapy, HIV; AIDS;
antisense; immune disorder; autoimmune disease; graft rejection;
graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and down-regulate the immune response in a
                                                                                                                                                                                                                                                                                   /product= "Human bcl-XL protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 51-52; 76pp; English
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTCAACCAGTCCATTGTCCA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00435518.
95US-00481739.
                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US006203
(first entry)
                                                                                                                                                                                                                                            135. .836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USNA ) US SEC OF NAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June CH, Thompson CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-506159/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 20; Conserv
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                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1996;
                                                                                                                                                                                                                                                                                                                                WO9634956-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               34-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
30-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1996.
                                           Bcl-XL gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis)
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AAZ93614/c ID AAZ936 XX AC AAZ936 XX

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Controlling cell behavior, useful e.g. for treatment of tumors, by modulating processing, e.g. splicing, of specific mRNA sequences with non-cleaving antisense agents.
                                                                                                                                                                                                                                                                                                                                                                             The invention relates to controlling cell behaviour by modulating the processing of a selected wild-type mRNA target in the cell, is new. The mRNA is bound to a specific-binding antisense compound that does not cleave bound mRNA. The antisense oligonucleotides are useful as research reagents, diagnostic agents (in hybridisation assays), and for treatment or prevention of diseases, e.g. to prevent or delay infections, inflammation and tumours. The present sequence is the cDNA for the human bcl-x which is a target for antisense oligonucleotides if the invention
                                                                                                                                                                                                                                Monia BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                         Human; antisense; IL-5R; bcl-x; ss; antiinfection; antiinflamatory;
cytostatic; inflammation; infection; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Bcl-2; Bcl-xL; Bax; VDAC; apoptosis inhibitor; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                              Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 4; Length 926; 100.0%; Pred. No. 5.2; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                Wyatt JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Bcl-xL nucleotide sequence SEQ ID NO:3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                Manoharan M,
                                                                                                                                                                                                                                                                                                                                                     Example 15; Page 113; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis promoter; diagnosis; ss.
                                                                                                                                                                                                                  Crooke ST, Manc...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTCAACCAGTCCATTGTCCA
                                                                                                                                               28-MAR-2000; 2000WO-US008174.
                                                                                                                                                                          28-MAR-2000; 2000WO-US008174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                          Mckay R,
                                                                                                                                                                                                                                                                      WPI; 2001-626250/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Human bcl-x cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2000287689-A.
                                                                                          WO200172765-A1
                                                                                                                                                                                                                             CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2001
                                                                                                                     04-OCT-2001
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                                                                                                                                                                                                                                             Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
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                                                                                                                                                                                                                                Bennett
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inhibitor or an apoptosis promoter in which VDAC-liposome, an index substance which can pass VDAC and a sample are incubated and the change in the concentration of the index substance during the incubation is detected to judge the presence of apoptosis inhibition or apoptosis promotion. The apoptosis inhibitor or the apoptosis promoter can be used as a drug and a diagnostic agent for various diseases caused by apoptosis inhibition or apoptosis promotion. The present sequence encodes the human Bcl-xL protein, which is an apoptosis inhibitor used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                                                                            present invention describes a method for screening for an apoptosis
                                                  drug and a diagnostic agent for various diseases caused by apoptosis inhibition or apoptosis promotion.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to detecting (M1) granulocyte (GC) activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozcal infection; fungal infection; sterile inflammatory disease; psoriasis; rhematoid arthritis; glomerulonephritis; acthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA differentially expressed in granulocytic cells #1337.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 926;
                                                                                                                                                                                                                                                                                                                                                             Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; 100.0%; Pred. No.
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                                                                                                                         Claim 16; Page 14-15; 22pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTCAACCAGTCCATTGTCCA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK84766 standard; cDNA; 926
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Best Local Similarity 100.
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2001-065575/08
                  P-PSDB; AAB50538
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WPI; 2003-140617/13.

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CGCAA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC. where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammatory disease, by contacting a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammation disease, by contacting a tissue having inflammation with an agent capable of modulating GA, M3 is useful for detecting GCA, M2 is useful for modulating GA, M3 is useful for detecting an agent capable of modulating GA, m3 is useful for detecting an attissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammation disease, inflammation disease, m4 is useful for detecting an inflammatory disease, or subject to a pathogen or sterile inflammation for subject, exposure of a subject to a pathogen or sterile inflammation and tissue, m4 is useful for detecting an inflammatory disease, contacting an inflammatory disease, condition, viral infection, parasitic infection, protozoal infection, creption and m3 is useful for reatine gene differentially conditions. The present sequence represents a gene of the above conditions. The present expersence in a subject in the present 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-tumour; DNAzyme; bcl-2 gene; tumour; malignant; chemotherapy; radiation therapy; catalytic domain; enzyme; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in granulcoytes. Note: The sequence data for this pate not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.
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ID ABT16641 standard; DNA; 926
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Best Local Similarity
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The invention relates to a DNazyme which specifically cleaves mRNA transcribed from a member of the bcl.2 gene family. The DNazymes comprise a catalytic domain, binding domains contiguous with the 5' and 3' end of the catalytic domain, and therefore hybridise with, the two regions immediately flanking the purine residue of the cleavage site within the bcl.2 gene family mRNA, at which DNAzyme-catalysed cleavage site within the branaceutical composition comprising a DNAzyme of the invention is useful for treating tumours in a subject, and for enhancing the sensitivity of malignant or virus infected cells infected cells to therapy. The DNAzymes are useful in diagnostics, therapeutics, prophylaxis, research agents and in kits. The DNAzymes are also useful to increasing the susceptibility of tumour cells to anti-tumour therapies such as chemotherapy and radiation therapy. This polynucleotide sequence represents a human bcl-2 gene of the invention
                                  Novel DNAzyme useful for treating tumors, and for enhancing the sensitivity of malignant or virus infected cells to therapy, comprises catalytic domain and binding domain contiguous to the catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a hamster host cell or a murine myeloma cell genetically modified by introducing nucleic acid sequences that encode for an anti-apoptosis gene, a selectable amplifiable marker gene or at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genetically modified host cells comprising nucleic acid sequences that encode for an anti-apoptosis gene, a selectable amplifiable markegene or at least one gene, useful for producing biopharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic, murine myeloma cell; anti-apoptosis ;
biopharmaceutical protein; bcl-xL; apoptosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human bcl-xL nucleic acid sequence #SEQ ID 1.
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                                                                                                               Disclosure; Page 44; 67pp; English
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Best Local Similarity 100.
Matches 20, Conservative
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                      least one protein encoded by a gene of interest, particularly for the production of biopharmaceutical proteins. The genetically engineered host cells have improved survival properties and enhanced level of active anti-apoptosis genes compared to non-transfected as well as non-amplified parental cells. The current sequence represents a bcl-xL nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia; retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic; Alzheimer; disease; Parkinson's disease, amyotrophic lateral sclerosis; acquired immune deficiency syndrome; neurodegenerative disorder; AIDS; nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective;
The cells are useful for the production of at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compound useful for treating reduced apoptotic conditions e.g. cancer comprises nucleobases targeted to nucleic acid molecule encoding human
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 10; Length 926; 100.0%; Pred. No. 5.2;
                                                                                                                                                                                                                                            Sequence 926 BP; 220 A; 249 C; 264 G; 193 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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/product= "Human bcl-x protein"
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                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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26-MAR-1999; 9US-00277020.
02-UIW-1999; 9US-003743.
12-DEC-2000; 2000US-00734846.
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   one gene of interest.
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MONIA B P.
NICKOLOFF B J.
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                                                                                                                                                                                   sequence.
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                                                                                                                                                                                                                                                                                                         Query Match
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(ZHAN/)
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(MONI/)
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least
least
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AAD64187/
ID AAD6
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The present invention relates to methods for modulating the expression of bcl-x. The invention is useful for sensitising cancer cells such as

Claim 1; SEQ ID NO 1; Opp; English

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glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention is useful for treating acquired immune deficiency syndrome (AIDS), neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy and ischaemia such as myocardial infarction and stroke. The present sequence is human bcl-x DNA
                                                                                                                                                                                                                                                                                     Gaps
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D30746 Homo sapien
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U51277 Mus musculu
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U51278 Mus musculu
BD012974 A mutagen
BD013799 Modified
U72350 Rattus norv
AX827805 Sequence
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Z23115 H.sapiens b
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BD243042 Antisense
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E58777 Screening m
I52011 Sequence 5
AR371661 Sequence
AR380885 Sequence
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PR 02-JUL-1998 US 09/109614
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/mol_type="genomic DNA"
/do_xref="taxon:32630"
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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PR 02-JUL-1999 JP 2000557839
PP C12M15-1999 JP 2000557839
PP C12M15-1999 JP 2000557839
PP C12M15/09.AG1K9/127,AG1K9/127,AG1K31/712,AG1K31/7125, PC
AG1K47/42
PC AATLAY A2.
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Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.
AY263337
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I (bases 1 to 137)

Yang, H., Sadda, M. and Lu, S.
5'-alternative splicing of BCLX in HepG2
Unpublished

2 (bases 1 to 137)

Yang, H., Sadda, M. and Lu, S.
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/db_xref="taxon:32630"
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Patent: JP 2002519048-A 15 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/15
                                                                                                                                                                                                                                                                                                                                     Oligonucleotide inhibitors of bcl-xL
Patent: JP 2002519048-A 14 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/14
PD 02-JUL-2002
PP 02-JUL-1999 JP 2000557839
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AGIK47/48, AGIK48/00, AGIP35/00, CI2N15/00
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/organism="synthetic construct"
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JP 2002519048-A/15.
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Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced.
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T. (bases 1 to 328)
Yang, H., Sadda, M. and Lu, S.
S.-alternative splicing of BCLX in HepG2
Direct Submission
Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los
Angeles, CA 90033, USA
Location/Qualifiers
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Yang, H., Sadda, M. and Lu, S.
Direct Submission
Submitted (26-WAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los Angeles, CA 90033, USA
Location/Qualifiers
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58;
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                                                        1. 137
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/cell_line="HepG2"
/135. .>137
/note="BCLX; alternatively spliced"
/prodon_statt=1
/product="BCL211"
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/codon_start=1
/product="BCL2L1"
                                                                                                                                                                                                                                                                                    0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HepG2"
326._>328
                                                                                                                                                                                   /protein_id="AAP22029.1"
/db_xref="G1:30349285"
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/db_xref="G1:30349283"
/translation="M"
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Homo sapiens
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Best Local Similarity 100.
Matches 20; Conservative
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Matches 20; Conserve
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RESULT 6 AY263335/c

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Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 388)

Yang, H., Sadda, M. and Lu, S.

2 "Alternative splicing of BCLX in HepG2
Unpublished
2 (bases 1 to 388)

Yang, H., Sadda, M. and Lu, S.

Direct Submission -
Submitted (26-MAR-2003) Medicine, GI/Liver, 2011 Zonal Ave, Los
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AY263335 388 bp mRNA linear PRI 03-MJ
Homo sapiens BCL2L1 mRNA, partial cds, alternatively spliced
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Pred. No. 52;
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CQ727769
CQ727769.1 GI:42294740
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/mb_xref="taxon:9606"
/cell_line="HepG2"
386._>388.
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/db_xref="G1:30349281"
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Location/Qualifiers
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Location/Qualifiers
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/product="BCL2L1"
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                                                                 AY263335.1 GI:30349280
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 8 AR054022/c

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PAT 12-SEP-2003
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Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1458 19-AUG-2003;
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To lases 1 to 737)

R Thompson, C.B., Boise, L.H. and Nunez, G.

Nettebrate apoptosis gene: compositions and methods
Vertebrate apoptosis gene: compositions and methods
Vertebrate apoptosis.

All Patent: US 6395510-A 7 28-MAY-2002;

Location/Qualifiers
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                                                                                                                                        6; Length 737;
Vertebrate apoptosis gene: compositions and methods
Patent: US 5646008-A 7 08-JUL-1997;
Location/Qualifiers
1. .737 /organism="unknown"
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches
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Sequence 7 from patent US 6395510.
AR371662
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/organism="unknown"
/mol_type="genomic DNA"
                                                                                     /mol_type="unassigned
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116 CTCAACCAGTCCATTGTCCA 97
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AR380913.1 GI:40088547
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AR380913/c
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AR371662/c
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                                                                                                                                                                                                     Unclassified.

1 (bases 1 to 737)
Thompson, C.B., Boise, L.H. and Nunez, G.
Vertebrate apoptosis gene: compositions and methods
Patent: US 5834309-A 8 10-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; Score 20; DB 6; Length 737; Similarity 100.0%; Pred. No. 49; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thompson, C. B., Boise, L. H. and Nunez, G.
Thompson, C. B., Boise, L. H. and Nunez, G.
Vertebrate apoptosis gene: compositions and methods
Patent: US 6303331-A 8 16-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 6; Length 737, 100.0%; Pred. No. 49;
                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                        DNA
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1 (bases 1 to 737)
Thompson, C.B., Boise, L.H. and Nunez, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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Sequence 7 from patent US 5646008.
152012
                                                                                     AR054022 737 bp
Sequence 8 from patent US 5834309.
AR054022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR172595 737 bp
Sequence 8 from patent US 6303331.
AR172595 GI:17912086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTCAACCAGTCCATTGTCCA 20
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   116 CTCAACCAGTCCATTGTCCA 97
                                                                                                                                        AR054022.1 GI:5978884
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Unclassified.
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Best Local Similarity
Matches 20; Conserv
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116

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RESULT 9 AR172595/c

DEFINITION

LOCUS

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VERSION KEYWORDS

source

DRIGIN

Matches

JOURNAL FEATURES

TITLE

DEFINITION

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RESULT 10 I52012/c

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2 (based 1) MAT

2 (bases 1 to 737)

Furka, L.A., Mao, X., Nunez, G. and Thompson, C.B.

Dol's, a Mol. 2-related gene that functions as a dominant regulator cell death

Cell 74 (4), 597-608 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA80662.1"
| Datein_id="CAA80662.1"
| Datein_id=101:63237"
| Datein_id=201:07817"
| Abtein=10n="MSGSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESE
| Aranslation="MSGSNRELVVDFLSYKLSQKGYSWSGFSDVEENRTEAPEGTESE
| RapebalrogniitpedtaygsPeQDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLGSLFSRK"
                                                                           PRI 12-JAN-1995
                                                                                                                                                                                                                                           Direct Submission
Submitted (22-JUN-1993) Craig B Thompson, Howard Hughes Medical
Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-7AN-1995) Craig B Thompson, Howard Hughes Medical Institute, University of Chicago, 5841 South Maryland, Chicago, IL, 60637, USA
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                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 737)

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On Jan 13, 1995 this sequence version replaced gi:510902.
Location/Qualifiers
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Pred. No. 49;
Mismatches 0; Indels
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                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="bcl-x8"
(cell type="peripheral blood T cell"
(dev gtage="Adult"
135. .647
                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                         737 bp
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100.0%; Pr
tive 0;
 116 CTCAACCAGTCCATTGTCCA
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gene="bcl-xS"
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                                                                                      H.sapiens bcl-xS mRNA.
223116 L20122
223116.1 GI:623236
bcl-xS gene.
                                                                                                                                                 Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 20; Conserv
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TITLE
JOURNAL
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                                            RESULT 13
HSBCLXS/c
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.

E. 1 (Dases 1 to 766)

Murray,J.F., Dong,Y.B., Leigh,A.J., Scaramuzzi,R.J. and Carter,N.D. Bcl.x in the sheep ovary

Unpublished

E. 2 (Dases 1 to 766)

Murray,J.F., Dong,Y.B., Leigh,A.J., Scaramuzzi,R.J. and Carter,N.D. Direct Submission

Direct Submission

Loration/Oualitiers

Hospital Medical School, Cranmer Terrace, London SW17 ORE, UK
                                                                                                                                                                                                                                                  Hardwick, J.M.
Direct Submission
Submitted (13-JUN-1994) J. Marie Hardwick, Neurology, Johns Hopkins School of Medicine, 600 North Wolfe St., Baltimore, MD 21287-7681, School of Medicine, 600 North Wolfe St., Baltimore, MD 21287-7681, NSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RETPSAINGNPSWHLADSPEVNGATGHSSSLDAREVI PWAAVKQALREAGDEFELRYR
REFBLILTSOLHITPGTAYQSPEQVYNELFRDGVNWGRI VAFFSFGGALCVESVDKEMQ
VLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGGERFNRWFLTGM
TVAGVYLLGSLFSRR
                                                                                                                        1 (bases 1 to 764)
Wesselingh, S.L., David, G.L., Choi, S., Veliuona, M. and Hardwick, J.M.
Cloning and expression of rat bcl-x in cultured neurons
Unpublished
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                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Ovis aries Bcl-x long protein mRNA, complete cds.
AF164517
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol type="unassigned DNA"
/db_xref="taxon:10116"
/tissue type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB
llarity 100.0%; Pred. No. 49;
Conservative 0; Mismatches
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/db_xref="GI:505699"
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/tissue_type="ovary"
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                        Rattus norvegicus
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Query Match
100.0%; Score 20; DB 4; Length 766;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 CTCAACCAGTCCATTGTCCA 20
Db 22 CTCAACCAGTCCATTGTCCA 3

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Search completed: February 4, 2005, 23:30:32 Job time : 485.738 secs

BY220922 UI-M-BH2. BY329071 BY191347 BY181507 BY209882

BY191347

BY176914 BB869154 BY353250

BY219527 BY219527 AA232598 BY176914

BY016163 BY180189

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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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                                                                           Mus musculus
OmniBank
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BE728507 601561960
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                                              2005, 20:41:45; Search time 2384.67 Seconds (without alignments) 305.616 Million cell updates/sec
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BF026532
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      5.1.6
Compugen Ltd.
                                                                                                                             32822875 segs, 18219865908 residues
                                                                                                                                          Total number of hits satisfying chosen parameters:
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      GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                 sw model
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BM049633
BE560320
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BF688810
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BF128036
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gb_htc::*
gb_est3::*
gb_est5::**
gb_gs81::*
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                                 nucleic search,
            Copyright
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GSS 02-OCT-2003
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                                                                                                                                                                                                                                                    AMGNNUC:M
BB870590
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 136)
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OST289185 Mus musculus 129Sv/Ev Mus musculus genomic clone
OST289185, genomic survey sequence.
BY333899
BB869154
BY353250
BY010071
BY016163
BY180189
BY180189
BY180189
BY180646
CB8133646
CB8130646
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
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Pred. No. 33;
0; Mismatches 0; Indels
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/organism="Mus musculus"
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/strain="1295v/Ev"
/db_xref="taxon:10090"
/clone="0ST29198"
/cell type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
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                                                                                                                                                                                                                     BY180646
CB813589
BB870590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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Homo sapiens (human)
Homo sapiens
                                                                  Unpublished (1999)
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BF688810
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nes 20; Conserv
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                   AUTHORS
TITLE
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AUTHORS
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//db_xref="ntaxon:9606"
/clone="INMERS:4653900"
/tlssue="INMERS:4653900"
/tlssue="INMERS:4653900"
/tlssue="INMERS:4653900"
/tlssue="INMERS:4653900"
/tlssue="Dype="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone=lb="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                         BG684338 114 MGC_48 Homo sapiens cDNA clone IMAGE:4763900 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1630 row: e column: 21
High quality sequence start: 6
High quality sequence stop: 122.
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo_sapiens"
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CTCAACCAGTCCATTGTCCA 79
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BE386533
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BG684338/c
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BE386533/c
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                                                                                                                                                   DEFINITION
                                                                                                                                                                                         ACCESSION
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KEYWORDS
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/mol_type="marker solutions" / mol_type="marker solutions" / mol_type="marker solutions" / mol_type="marker solutions" / done="lmAddE:3614708" / done="lmAddE:3614708" / done="lmAddE:3614708" / done="lmAddE:"DHIOB (phage-resistant)" / done="lmarker solutions" / lnb host="mild Mage of the good of the libe="lmarker solutions" / note="Corgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2: CoCRI; CDNA made by oligo-dT priming. Directionally cloned into BcoRI/KhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected > SOODp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 177)

                                                                                                                                                                                                                          CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM377 row: j column: 21 High quality sequence stop: 151.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
plate: LiCMA156 row: n column: 24
High quality sequence start: 2
High quality sequence store: 177.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Stausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
1 (Dases 1 to 101)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/organism="Homo sapiens"
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Homo sapiens (human)
Homo sapiens
                 20; Conservative
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Local 20; Conserva
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AA351198/c
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DEFINITION
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KEYWORDS
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/mol_type="mRNA"
/db xref="taxon:9666"
/clone="IMAGE:429479"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/clone=1bhost="DH10B (phage-resistant)"
/clone=1bhost="DH10B (phage-resistant)"
/clone=1bhost="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH-MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE407849 110L-2000 001300889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635255 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198)
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Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM331 row: b column: 24
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/mol_type="mRNA"
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High quality sequence stop: 198.
Location/Qualifiers
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/clone="IMAGE:3635255"
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Homo sapiens
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BE407849
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Best Local Similarity
Matches 20; Conserva
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BE407849/c
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Score 20; DB 2; Length 198; Pred. No. 35;

100.0%;

Best Local Similarity

Query Match

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EST58853 Infant brain Homo sapiens CDNA 5' end similar to apoptosis AA351198
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602461986F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4578596 5',
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I (bases I to 200.
Adame, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nat. Genet. 4, 373-380 (1993)
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9712 Medical Center Drive, Rockville, MD 20850 USA
9712 Medical Center Drive, Rockville, MD 20850 USA
9713 1018699056
Fax: 3018699423
Email: arkerlav@tigr.org
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/mol_type="mRNA"
/db_xref="ATCC (inhost):151593"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="infant"
/clone_lib="Infant brain"
/note="forgan: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 210)
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Pred. No. 35;
Mismatches 0; Indels
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Contact: Kerlavage, AR
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryogia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 213)

NIH-WGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP
                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1294 row: 1 column: 21
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Acranism="Homo sapiens"
// organism="MRNA"
// db_xref="taxon:9606"
// clone="IMAGE:45/8596"
// tissue_type="melanotic melanoma"
// lab_host="DH108" (phage-resistant)"
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High quality sequence stop: 213.
Location/Qualifiers
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/mol_type="mRNA"
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Location/Qualifiers
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Best Local Similarity
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BG478819/c
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DEFINITION
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VERSION
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AUTHORS
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                    TITLE
JOURNAL
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  AUTHORS
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                                                          COMMENT
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/clone="IMAGE:4643800"
/tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
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/tissue type="normal pigmented retinal epithelium"
/labhone="DHIOB (phage-resistant)"
/clone lib="NIH MGC 43"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG752203 218 bp mRNA linear EST 15-MAY-2001
602731335F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4874865 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1755 row: e column: 10
High quality sequence stop: 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 213; 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 CTCAACCAGTCCATTGTCCA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTCAACCAGTCCATTGTCCA 20
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
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RESULT 10 BE727284/c

ò 셤 DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

COMMENT

AUTHORS REFERENCE

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BE275637 227 bp mRNA linear EST 13-JUL-2000
601121162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988806 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 227)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArcC/DCTD/DTP
Tissue Procurement: ArcC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW829 row: n column: 22
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMOB row: k column: 15
                 NIH-WGC http://mgc.nci.nth.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 2; Length 225; 100.0%; Pred. No. 36;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                         High quality sequence start: 40 High quality sequence stop: 225. Location/Qualifiers
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High quality sequence stop: 227.
Location/Qualifiers
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  (bases 1 to 225)
                                                                      Unpublished (1999)
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BE275637
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Matches 20; Conserv
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BE275637/c
LOCUS
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AUTHORS
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JOURNAL
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COMMENT
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KEYWORDS
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                                                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="mediantic melanoma".
/lab host="BH10B (phage-resistant)"
/lab host="BH10B (phage-resistant)"
/lone=lib="NIH MGG_20"
/note="Organ: Skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into BCORI/KhoI sites using the following S;
adaptor: GGCACGAG(G). Size-selected 5500bp for average
insert size_1:8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 bp mRNA linear EST 10-OCT-2000 601672487F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955413 5', BP026532
                                                                                                                                                                                      BE727284 223 bp mRNA linear EST 15-SEP-2000 601560967F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3830416 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM504 row: f column: 17
High quality sequence start: 38
High quality sequence stop: 223.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 223)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 36;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGB:3830416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCAACCAGTCCATTGTCCA 138
                                                              132 CTCAACCAGTCCATTGTCCA 113
                      20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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                                                                                                                                                                                                                                           mRNA sequence.
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Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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source

FEATURES

RESULT 11 BF026532/c DEFINITION

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ORIGIN

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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Gaps

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0;

Query Match

DRIGIN

Matches

RESULT 13 BG489250/c

DEFINITION

SOURCE ORGANISM

AUTHORS TITLE JOURNAL REFERENCE

ACCESSION VERSION KEYWORDS

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/tissue type="leionyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH1 MGC 46"
/clone lib="NH1 MGC 46"
/noce="Organ: uferus; Vector: pOTB7; Site l: Xhol; Site 2:
EcoR1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Khol sites using the following 5' adaptor:
GGCACGAG(G): Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG746689 232 bp mRNA linear EST 15-MAY-2001 602704010F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857171 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 23). NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                    BF685843 22-DEC-20
602143136F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304288 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1169 row: g column: 09
Plate: LLCM1169 row: g column: 09
High quality sequence stop: 230.
Location/Qualifiers
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            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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         20; Conservative
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/clone="IMAGE:2988806"
/tissue_type="melanotic melanoma"
/tab.host="BH10B (phage-resistant)"
/clone=1ib="NH1M GGC_20"
/clone=1ib="NH MGC_20"
/cl
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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602518262F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4636935 5'
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Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Flate: LLCM196 row: k column: 16

High quality sequence stop: 228.
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Best Local Similarity
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FEATURES

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/clone="IMAGE:4857771"
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                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Nutional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procurement. ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing Dy: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIML at:
http://image.llni.gov
Plate: LLCM1709 row: d column: 04
High quality sequence stop: 232.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 232)

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/mol_type="mRNA"
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Search completed: February 5, 2005, 08:11:23 Job time: 2391.67 secs

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AX925690 Sequence
CQ139631 Sequence
CQ139631 Sequence
CQ222999 Sequence
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CQ38104 Sequence
AX925692 Sequence
AX925694 Sequence
AX925696 Sequence
AX92603131 Oryctolag
BD102202 Method of
BD102202 Method of
BD102208 Home sapi
U10101 Mus musculu
BT008248 Synthetic
AF216205 Sus scrof
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S76513 bcl-x=apopt
AR054022 Sequence
AR172595 Sequence
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Unclassified.
1 (bases 1 to 20)
Bennett, C. Frank., Cooke, S. T., Manoharan, M., Wyatt, J. R., Baker, B. F.,
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AF279286 Rattus no
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Bennett, C. Frank., Dean, N.M., Monia, B.P., Nickoloff, B.J. and
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Patent: US 6172216-A 21 09-JAN-2001;
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Sequence 42 from patent US 6210892.
AR144314
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/organism="unknown"
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BD102203 Method fo
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AR118505 Sequence
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BD235184 Oligonucl
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CQ816672 Sequence
AX017820 Sequence
BD17331 Different
AR176180 Sequence
BD178062 Stress-re
                                                                                           ); Search time 480.738 Seconds (without alignments)
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AR144314 Sequence
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Stein, C.A.
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PI CY A STEIN
PC
CI2NIS/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC
Monia, B.P., Freier, S.M., McKay, R. and Karras, J.G.
Alteration of cellular behavior by antisense modulation of mRNA
processing
Patent: US 6210892-A 42 03-APR-2001;
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Patent: JP 2002519048-A 2 02-JUL-2002;
THE TRUSTESS OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/2
PD 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
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A61K47/48,A61K48/00,A61P35/00,C12N15/00
ANTISENSE OLIGONUCLEOTIDE
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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BD2351501 GI:33044920
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                                                                      1. .20
/organism="unknown"
/mol_type="unassigned DNA"
                                                       Location/Qualifiers
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JP 2002519048-A/16.
synthetic construct
synthetic construct
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artificial sequences.
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A61K47/°
PC A67
CC A<sup>V</sup>
FH FT
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Datent: JP 2002519048-A 36 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
S Artificial Sequence
PN JP 2002519048-A/36
PN 02-JUL-2002
PP 02-JUL-1999 JP 2000557839
PR 02-JUL-1999 US 09/109614
PI CY A STEIN
PC CLOALS/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
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C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
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Digonuclectide inhibitors of bcl-xL
Patent: JP 2002519048-A 16 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS. Artificial endece
PN JP 2002519048-A/16
PD 02-JUL-1999 JP 2000557839
PR 02-JUL-1999 US 09/109614
PI CY A STEIN
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PC AAINTSENSE OLIGOUCLEOTIDE
CC ANTISENSE OLIGOUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
FH Key
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PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC PRIMER Location/Qualifiers
FT source 1.20
/organism='Artificial Se
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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3.9;
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misc_binding (7). (8)
misc_binding (10). (13)
misc_binding (17). (20).
Location/Qualifiers
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100.0%; Score 20;

Best Local Similarity 100.0%; Pred. No. Matches 20; Conservative 0; Mismatch
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synthetic construct
artificial sequences.
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Best Local Similarity
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C12N5/10//
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C12N15/09,A61K9/10,A61K31/337,A61K31/711,A61K31/7115,A61K31/
                                                                                                                                                                                                                                                                                         synthetic construct
synthetic construct
artificial sequence.
1 (bases 1 to 20)
Bennetr, F.C., Dean,N.M., Monia,B.P., Nickoloff,B.J. and Zhang,Q.
Antisense modulation of bcl.x expression
FSIS PARMARCHACHOS INC
OS Artificial Sequence
DY 2002526093-A/20
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                                                                  Length 20;
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28-SEP-1999 JP 2000574543
07-OCT-1998 US 09/167921,26-MAR-1999 US 09/32743
                                                                                                                                                                                                                                     Antisense modulation of bcl-x expression,
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    .20
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/db_xref="taxon:32630"

                                                                   DB 6;
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Sequence 13 from Patent WO2004040018.
CQ816672.1 GI:48144938
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                                                                 100.0%; Score 20; 100.0%; Pred. No.
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JP 2002526093-A/20.
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synthetic construct
artificial sequences.
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Qualitative differential screening
Patent: WO 9946403-A 13 16-SEP-1999;
BRACCO LAURENT (FR), TOCQUE BRUNO (FR); EXONHIT THERAPEUTICS S. (FR); SCHWEIGHOFFER PABIEN (FR)
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Tocque, B., Bracco, L., Edon, F. and Schweighoffer, F. Qualitative differential screening
Patent: WO 2004040018-A 13 13-MAY-2004;
Exonhit Therapeutics S.A. (FR)
Location/Qualifiers
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artificial sequences.

1 (bases 1 to 24)
Schweighoffer,F., Bracco,L. and Tocque,B.
Differential screening
EXONHIT THERAPEUTICS SA
OS Artificial Sequence
BN JP 2002505887-A/12
PD 26-FEB-2002
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/organism="synthetic construct"
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/db xref="taxon:32630"
/noTe="OLIGO"
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/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/note="oligo"
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AX017820
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JP 2002505887-A/12.
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synthetic construct
artificial sequences.
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1 (bases 1 to 30)
Yuko,O., Ichiro,M. and Camal,A.M.
Stress-tolerant plant having cell death inhibitory gene transferred
thereinto and method for constructing the same
Patent: JP 2000023583-A 6 25-JAN-2000,
NATL INST OF AGROBIOLOGICAL RESOUCES
OS Artificial Sequence
PN JP 2000023883-A/6
PD 25-JAN-2000
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                                                                                                                                   Topology:
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                                                                                                                                                                                Stress-resistant plant having cell-death inhibitory gene
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  Unidentified
JP 2002300822-A/6
15-0CT-2002
10-FEB-2002 JP 2002026196
YUKO OHASHI,ICHIRO MITSUHARA,CAWAL A MALIK
A01HS/00,C12N15/09//C12N5/10,C12N15/00,C12N5/00 CC
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Location/Qualifiers
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/mol_type="genomic DNA"
/db zref="taxon:32644"

    30
    /organism="synthetic co
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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JP 2000023583-A/6.
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Best Local Similarity 100.
Matches 20; Conservative
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Linear;
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PF 11-MAR-1999 JP 2000535770
PR 11-MAR-1998 FR 98/02997
PR 11-MAR-1998 FR 98/02997
PR 14-MAR-1998 FR 98/02997
PR 15BIEN SCHWEIGHOFFER, LAURENT BRACCO, BRUNO TOCQUE PC C1201/68, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12NS/10 PC C12NS/00, C12N1S/00, C12N1S/00, C12N1S/00, C12N1S/00, C12N1S/00 C1
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Ohashi,Y., Mitsuhara,I. and Malik,C.A.
Stress-registant plant having cell-death inhibitory gene
transferrated thereinto and method of constructing the same
Patent: JP 2002300822-A 6 15-OCT-2002;
NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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AR176180
AR176180.1 GI:17917479
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JP 2002300822-A/6.
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Query Match 100.0%; Score 20; DB 6; Length 37; Best Local Similarity 100.0%; Pred. No. 3.8; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                            Conservative
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Job time: 484.738 secs
                                                                                                         Similarity
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Matches 20;
                                                                                            Query Match
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synthetic construct
artificial sequences.

1 (bases 1 to 31)

Kato, S., Equchi, C., Nagata, N. and Otake, M.
Method for detecting protein-protein interaction

Patent: WO 0168885-A 8 20-SEP-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP, SEISHI KATO, CHIKASHI EGUCHI, NAOKI
                                                            PAT 27-AUG-2002
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SEISHI KATO, CHIKASHI EGUCHI, NAOKI NAGATA
CI2N15/09,C12Q1/02//C07K14/47, (C12N15/09,C12R1:91), (C12Q1/02,
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PN WO 016885-A/8
PD 20-SEP-2001
PP 13-MAR-2001
PF 13-MAR-2001
PR 15-MAR-2000 JP 00P 073095, 24-AUG-2000 JP 00P 254418 PI
SEISHI KATO, CHIRASHI EGUCHI, NAOKI NAGATA, MIYAKO OTAKE PC
C12N15/79, G01N13/68/C12P21/02, C07K19/00
CC Synthesized Oligonucleotide
FH Key Location/Qualifiers
FT source 1. .11
/organism='Artificial Sequence'.
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Location/Qualifiers
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                                                31 bp DNA linear Method of detecting protein-protein interaction. BD084109
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Method for detecting protein-protein interaction.
BD102203
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synthetic construct
artificial sequences.

1 (bases 1 to 31)
Kato, S., Equchi, C. and Nagata, N.
Method of detecting protein-protein interaction
Patent: JP 2001327296-A 8 27-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                               Synthesized Oligonucleotide
Kev Location/Qualifiers

    .31
    forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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C12N15/00, (C12N15/00,C12R1:91)
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                                                                                                                                                                                                                                                                  Artificial Sequence
JP 2001327296-A/8
27-NOV-2001
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OS Artificial Sequence
PN WO 0168885-A/8
                                                                                                        BD084109.1 GI:22629719
JP 2001327296-A/8.
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WO 0168885-A/8.
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Best Local Similarity 100.0%
Matches 20, Conservative
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KEYWORDS
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ORGANISM
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TITLE
JOURNAL
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TITLE
JOURNAL
                         RESULT 13
                                                                                                                                                                                     REFERENCE
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Host cells having improved cell survival properties and methods to generate such cells
Patent: WO 03083093-A 19 09-OCT-2003;
Boehringer Ingelheim Pharma GmbH & Co. KG (DE)
Location/Qualifiers
                                                                                                                                                                        Gaps
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                                                                                                                         100.0%; Score 20; DB 6; Length 31; 100.0%; Pred. No. 3.9; or Mismatches 0; Indels
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32650"
/noTe="Oligonucleotid (Eco-Bcl for)"
1. .31
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                   37 bp 1 Sequence 19 from Patent WO03083093.
                                                                                                                                                                                                               1 TCCCGGTTGCTCTGAGACAT 20
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synthetic construct
artificial sequences.
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22 20 100.0 600 4 AAK35096 Aak35096 Human bon Aak09207 Human bra Abga484 Human bra Abga484 Human bra Abga484 Human bra Abga484 Human liv Abga9858 Human gen Adh52636 Chinese h Adh52636 Chinese h Adh52640	24 6 24 6	PF 02-JUL-1999; 99WO-US015250. XX PR 02-JUL-1998; 98US-00109614. XX XX XX YX
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: February 4, 2005, 15:50:53; Search time 258.033 Seconds (without alignments) 1	Database: N_Geneseq_23Sep04:* 1: geneseqn1990s:* 2: geneseqn190s:* 3: geneseqn2000s:* 4: geneseqn2001bs:* 5: geneseqn2001bs:* 6: geneseqn2001bs:* 7: geneseqn2003ss:* 9: geneseqn2003ss:* 10: geneseqn2003ds:* 11: geneseqn2003ds:* 12: geneseqn2004s:* and is derived by analysis of the total score distribution.	No. Score March Length DB ID

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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpytyidyl)porphine and/or tetra meso- (antihium)porphine; in pharmaceutical compositions, useful as above. Sequences ARZ46971-983 represent antisense oligos specific for the bcl-X1 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function). The antisense oligonucleotides may have a therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-x; bcl-xs; antisense; therapy; apoptosis; splice site;
cell signalling molecule; ultraviolet radiation; UV; cancer;
                                                                                                                                                                                                                                     100.0%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 1.7; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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AAZ8

XXX AAZ8

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DB 3; Length 20;

100.0%; Score 20;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to controlling cell behaviour by modulating the processing of a selected wild-type mRNA target in the cell, is new. The mRNA is bound to a specific-binding antisense compound that does not cleave bound mRNA. The antisense oligonucleotides are useful as research reagents, diagnostic agents (in hybridisation assays), and for treatment or prevention of diseases, e.g. to prevent or delay infections, inflammation and tumours. The present sequence is an antisense oligonucleotide which targets the gene for human bcl-x
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "2' methoxyethoxy residues when 16-20 are also 2' methoxyethoxy residues. All cytosines in this region are also 5-methyl-cytosine"
16. .20
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                Gaps
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antiinfection; antiinflamatory; cytostatic; inflammation; infection;
tumour; ISIS 15999; probe.
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                Indels
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Mckay R, Karras JG;
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 Pred. No. 1.7;
              Mismatches
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/*tag= b
/mod_base= OTHER
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/mod_base= OTHER
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100.08;
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Best Local Similarity
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              Matches
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regulator of apoptosis. The invention includes a method of inhibiting the
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*tag=
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BAKER B F.
MONIA B P.
MCKAY R.
KARRAS J G.
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                                                                                                                                                                                                                                                            Local Similarity
les 20; Conserv
                                                                                                                                                                              human bcl-x gene
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(BAKE/)
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THE STATE OF THE S
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                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotide; bcl-x; human; apoptosis; inflammation; cancer; glioblastoma; leukaemia; autoimmune disorder; Alzheimer's disease; neurodegenerative disorder; AIDS; Parkinson's disease; phosphorothioate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense compound, 8 to 30 nucleobases in length, targeted to a nucleic acid molecule encoding a human bcl-x, useful for preventing or treating tumor formation, infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to antisense oligonucleotides which are between and 30 nucleobases in length and are targeted to a nucleotide sequence encoding human bcl-x. Human Bcl-x functions as a bcl-2-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "2'-O-methoxyethyl (2'-MOE) nucleotides, where cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotides, where
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Phosphorothioate internucleotide linkage
                                              ö
               Length 20;
                                                                                                                                                                                                                                                                                            Human bcl-x antisense chimeric oligonucleotide SEQ ID 21.
                                              0; Indels
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/note= "2'-0-methoxyethyl (2'-MOE) nucle:
cytidine residues are 5-methylcytidines"
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                 4;
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             DB 4
                                              Mismatches
             Score 20;
Pred. No.
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            100.0%; Sc
100.0%; Pr
:ive 0;
                                                                                            TCCCGGTTGCTCTGAGACAT
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99US-00277020.
99US-00323743.
                                                                           1 TCCCGGTTGCTCTGAGACAT
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                                                                                                                                                                                          AAH27678 standard; DNA; 20
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                                              Conservative
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*tag=
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MONIA B P.
NICKOLOFF B J.
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        Query Match
Best Local Similarity
Matches 20; Conserv
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modified_base
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26-MAR-1999;
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(MONI/)
(NICK/)
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AAH27678
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expression of bcl-x in human cells or tissues through antisense inhibition by the antisense oligonucleotides. An antisense compound containing the oligonucleotide together with a chemotherapeutic agent is useful for preventing or treating tumour formation. The antisense compound is also useful for treating tumour formation infection or inflammation. Cancer particularly glioblastoma and leukaemia, autoimmune disorders and viral infections, AllS, neurodegenerative disorders like Alzheimer's or Parkinson's diseases may be treated using compounds containing the antisense oligonucleotides. The present sequence represents an antisense oligonucleotide targeted against a region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note== "nucleotides 1-5 and 16-20 are 2'-methoxyethoxy (2'MOE); all 2'MOE cytosines are 5-methyl-cytosines; all linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Controlling cell behavior by modulating mRNA modification, useful in therapeutics and as research tool, comprises using antisense oligonucleotide which hybridize to mRNA and block modification regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense therapy, antisense oligonucleotide, apoptosis, mitosis differentiation, stress, hormone, cytokine, signalling molecule, mRNA modulation, mRNA cleavage, therapeutic, human, bcl-x, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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in vivo or in vitro.

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The invention relates to the control of cell behaviour by modulating the processing of a wild-type mRNA target, comprising binding to the target does not antisense compound which specifically hybridises to the target and does not elicit cleavage of the mRNA upon binding. The method of the invention can be used in therapeutics (i.e antisense therapy), including prophylaxis, and as a research tool. It is used for controlling the behaviour of a cell (especially responses such as apoptoasis, mitosis, differentiation and quiescence to stimuli such as stress, hormones, cytokines and other signalling molecules), tissue or organism through a human bcl-x equence represents a human bcl-x exon 1/exon 2 antisense oligonucleotide designated SEQ ID 42, designed to target areas of exon 1 and exon 2 of human bcl-x, particularly around the exon 1/exon 2 splice site and in sequence regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating diseases with oligonucleotides or interfering RNA, useful e.g. for cancer or autoimmune diseases, covalently coupled to mobile proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein; cytostatic; immunosuppressive; vitrucide; anti-HVV; antibacterial; cardiant; hyperproliferation; cancer; haematological; metastatic; autoimmune disease; infection; endocrine; neural; cardiovascular; autoimmune disease; infection; endocrine; neural; cardiovascular; pulmonary; repreductive system disorder; endocrytosis; metabolic process; murine; intracellular adhesion molecule 1; ICAM-1; antisense oligonucleotide; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 6; Length 20; 100.0%; Pred. No. 1.7; ive 0; Mismatches 0; Indels
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/note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
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                                       Example 14; Page 28; 50pp; English.
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/mod base= OTHER
                                                                                                                                                                                                                                                                                                                        present in bcl-xl but not bcl-xs
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 such as splice acceptor sites.
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Matches 20; Conservative (
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Gaps

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The present invention describes a method for treating a disease by administering: (a) a therapeutic oligonuclectide (TON) or double-stranded RANA (EMRNA) that includes a reactive group (RG) that can react with a combine protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or Gescribed: (1) TON of 15-30 bases that includes (1) a part that binds to target RNA or DNA and (15-30 bases that includes a part that binds to target RNA or DNA and is conjugated to MP through a covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is conjugated to MP through a covalent link. TON have Cytostatic, immunosuppressive, virucide, anti-HIV, antibacterial and cardiant conjugated to MP through a covalent link and particularly cancers, solid or haematological, including prevention of particularly cancers, solid or haematological, including prevention of metastatic spread); autoimmune diseases, viral or bacterial infections; candorrine, neural, cardiavascular, pulmonary or reproductive system disorders Also where TON or dsRNA are labelled, they can be used for disorders and monitoring of therapy. When linked to a mobile protein, conjugances (1) increased resistance to nuclease), without loss of affinity for the target. In many cases immune response to TON/dsRNA is also reduced, as is non-specific binding to endogenous proteins. The present sequence represents a human bol-xl antisense conjugantical proteins. The present sequence represents a human bol-xl antisense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retinitis pigmentosa; myocardial infarction, neuroprotective, cytostatic, acquired immune deficiency syndrome; neurodegeneralisclerosis; acquired immune deficiency syndrome; neurodegenerative disorder; AIDS; nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective; stroke; antisense; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia;
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/note= "2'-0-methoxyethyl (2'-MOE) nucleotides; All
cytidines are 5-methyl cytidines"
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1. .20
/*tag= a
                                      Claim 128; Page 12; 42pp; English.
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nes 20; Conserv
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(DEAN/) 1 (MONI/) 1 (NICK/) 1 (ZHAN/) 2

BENN/)

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The present invention relates to methods for modulating the expression of bcl-x. The invention is useful for sensitising cancer cells such as glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention is useful for treating acquired immune deficiency syndrome (ALDS), neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy and ischaemia such as myocardial infarction and stroke. The present sequence is human bcl-x antisense oligonucleotide. This sequence is the analogue of ISIS 15599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compound useful for treating reduced apoptotic conditions e.g. cancer comprises nucleobases targeted to nucleic acid molecule encoding human gene encoding intracellular membrane protein.
                  /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
/*tag= b
/mod_base= OTHER
/note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
cytosines are 5-methyl cytosines (5meC)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 10; Length 20; 100.0%; Pred. No. 1.7; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 21; Page 19; Opp; English.
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99US-00277020.
99US-00323743.
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MONIA B P.
NICKOLOFF B J.
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ses 20; Conserv
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        modified base
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                                                                                                                                                                                                                                                                                                                      07-OCT-1998;
                                                                                                                                                                                                                                                                                                                                        26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to methods for modulating the expression of bolls. The invention is useful for sensitising cancer cells such as glioblastoma and leukaemia to am apoptotic stimulus (e.g. ultraviolet radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention is useful for treating acquired immune deficiency syndrome (AIDS), neurodegenerative disorders such as Alrhemer's disease, Parkinson's disease, amyotrophic lateral sclerosis; retinitis pigmentosa, epilepsy and ischaemia such as myocardial infarction and stroke. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia; retinitis pigmentosa; myocardial infarction; neuroprotective; cytostatic; Alzheimer.'s disease; Parkinson's disease; amyotrophic lateral sclerosis; acquired immune deficiency syndrome; neurodegenerative disorder; AIDS; nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective; stroke; antisense; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compound useful for treating reduced apoptotic conditions e.g. cancer comprises nucleobases targeted to nucleic acid molecule encoding human gene encoding intracellular membrane protein.
/mod_base= OTHER
/note= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
cytidines are 5-methyl cytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bcl-x antisense oligonucleotide ISIS #17959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is human bcl-x antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Nickoloff BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
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99US-00277020.
99US-00323743.
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                                                                                                                                                         21-NOV-2002; 2002US-00302262
                                                                                                                                                                                                                                                      12-DEC-2000; 2000US-00734846
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                                                                                                                                                                                                                                                                                                                                                        В.
                                                                                                                                                                                                                                                                                                                                                                                                                    Dean NM,
                                                                                                                                                                                                                                                                                               BENNETT C F.
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NICKOLOFF F
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les 20; Conserv
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                                                                             US2003191300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    CF,
                                                                                                                                                                                                                  26-MAR-1999;
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Query Match

Matches

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Human; bcl-x; glioblastoma; leukaemia; chemotherapy; epilepsy; ischaemia; retilitis pigmentosa; mycoardial infarction; neuroprotective; cytostatic; Alzheimer's disease; Parkindal disease; amyotrophic lateral sclerosis; acquired immune deficiency syndrome; neurodegenerative disorder; AlDS;

Location/Qualifiers

sapiens

Ношо

Synthetic

epilepsy, ischaemia;

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The present invention relates to methods for modulating the expression of bcl-x. The invention is useful for sensitising cancer cells such as glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention is useful for treating acquired immune deficiency syndrome (AIDS), neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy and ischaemia such as myocardial infarction and stroke. The present sequence is human bcl-x antisense oligonucleotide. This sequence is the analogue of ISIS 15999
                                                               retinitis pigmentosa, myocardial infarction, neuroprotective, cytostatic, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis; acquired immune deficiency syndrome, neurodegenerative disorder, AIDS; nootropic, anticonvulsant, vasotropic, therapy, cerebroprotective; stroke, antisense, phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compound useful for treating reduced apoptotic conditions e.g. cancer comprises nucleobases targeted to nucleic acid molecule encoding human gene encoding intracellular membrane protein.
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/note= "2'-0-methoxyethyl (2'-MOE) nucleotides; All
cytosines are 5-methyl cytosines (5meC)"
                                                                                                                                                                                                                                                                                                         /notē= "2'-O-methoxyethyl (2'-MOE) nucleotides; All
cytosines are 5-methyl cytosines (5meC)"
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                                                    Human; bcl-x; glioblastoma; leukaemia; chemotherapy;
                  Human bcl-x antisense oligonucleotide ISIS #17791.
                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Phosphorothioate backbone"
16. .20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monia BP, Nickoloff BJ,
                                                                                                                                                                                                                                   Location/Qualifiers
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*tag=
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Best Local Similarity
Matches 20; Conserv
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MONIA B P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHANG Q Q.
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                                                                                                                                                                                Homo sapiens.
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26-MAR-1999;
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                                                                                                                                                                                                 Synthetic
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(NICK/)
(ZHAN/)
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%XCCCCCCCCCX8X414X6X1X454848X6X6X6X6X6X6X644444444444444444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to methods for modulating the expression of bcl-x. The invention is useful for sensitising cancer cells such as glioblastoma and leukaemia to an apoptotic stimulus (e.g. ultraviolet radiation, cancer chemotherapeutic drug (e.g. cisplatinum). The invention is useful for treating acquirted immune deficiency syndrome (AIDS), neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, epilepsy and ischaemia such as myocardial infarction and stroke. The present sequence is human bcl-x antisense oligonucleotide. This sequence is the analogue of ISIS 15999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compound useful for treating reduced apoptotic conditions e.g. cancer comprises nucleobases targeted to nucleic acid molecule encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                  /note= "2'-0-methoxyethyl (2'-MOE) nucleotides; All cytosines are 5-methyl cytosines (5meC)"
nootropic; anticonvulsant; vasotropic; therapy; cerebroprotective; stroke; antisense; phosphorothioate backbone; ss.
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100.0%; Pred. No. 1.7;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nickoloff BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene encoding intracellular membrane protein.
                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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99US-00323743
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Best Local Similarity lvv..
20; Conservative
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/*tag=
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MONIA B P.
NICKOLOFF B J.
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                                                                                                         Key
modified_base
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02-JUN-1999;
                                                      sapiens
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                                                                       Synthetic.
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(ZHAN/)
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(MONI/)
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RESULT 11

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Detection of protein-protein interactions for screening compounds capable of modifying the interaction comprises observing intracellular localization of one protein after altering the modification pattern.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer 1 used to amplify human apoptosis inhibitory factor Bcl-xL cDNA.
                                    Npw38; Npw8P; protein interaction; reporter function; eukaryotic cell; localization; protein network; intracellular; primer; amplify; PCR; polymerase chain reaction; mitochondria; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        random oligonucleotide library; protein interaction; ligand; receptor binding site; PCR; primer; ss; human; apoptosis inhibitory factor; Bcl-xL.
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                                                                                                                                                                                                                                                                                                                                             (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 30; 33pp; Japanese
  CDNA clone HP03564 ORF, primer P1
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                                                                                                                                                                                                                                         13-MAR-2001; 2001WO-JP001973.
                                                                                                                                                                                                                                                                                15-MAR-2000; 2000JP-00073095
24-AUG-2000; 2000JP-00254418
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                                                                                                                                                                                                                                                                                                                                                                                      Eguchi C,
                                                                                                                                                           WO200168885-A1.
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                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primers AAV57313 and AAV57314 were used to amplify the human bcl-xL (cell death suppressing gene) gene isolated from a human cDNA library. After amplification, the product was cloned into the EcoR1 site of pBluescript, thus obtaining the plasmid pM21. This plasmid, was used in the construction of an expression vector which can then be used in the preparation of a stress-resistant plant, by introducing this gene into a plant cell and then using this cell to regenerate a plant. The stress-resistant plant but been found to show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New stress-resistant transgenic plants, comprise cell death suppressing gene - used to confer resistance to stress caused by UV irradiation, super-oxide-generating herbicides or high salinity.
                                                                                                                                                                                                                                                                                                 Primer; PCR; amplification; bcl-xL; cell death suppressing gene; pM21; pBluescript; stress-resistant plant; UV irradiation; high salinity; superoxide-generating herbicide; ss.
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                                                                                                                                                                                                                                                          5' primer, used to amplify bcl-xL cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malik KA;
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AAV57313/C

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                                                                                                       Random oligonuclectide useful for detecting protein interaction, having base sequence, where each base of 1st and 2nd of the codon is the any of G, C, T (U), or A and the base of 3rd of codon is G or G, or G or T (U).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genetically engineered hamster or murine myeloma host cells comprising enhanced levels of active anti-apoptosis genes, useful for producing complex protein therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mammalian myeloma host cell; protein production; anti-apoptosis; cell death; Chinese hamster; bcl-xL; PCR; primer; ss; RT-PCR.
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                                                                                                                                                                                                                                                                                                      human apoptosis inhibitory factor Bcl-xL cDNA.
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                                                                                                                                                                  Example 2; SEQ ID NO 1; 43pp; Japanese.
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                                          (SERE-) SERESUTA REKISHIKO SCI KK
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            24-JUN-2002; 2002JP-00183456
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The invention relates to a novel mammalian host cell for producing protein therapeutics. The host cell comprises a hamster or a murine myeloma cell that is genetically modified by introduction of nucleic acid sequences encoding an anti-apoptosis gene, a selectable amplifiable

Example 5; SEQ ID NO 19; 46pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer; bcl-XS; PCR; polymerase chain reaction; bcl-XL; T-lymphocyte; activation; cell death; antibody; CD28 costimulation; gene therapy; HIV; AIDS; antisense; immune disorder; autoimmune disease; graft rejection; graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
marker gene and at least one gene of interest. The host cell of the invention may be useful for producing at least one protein encoded by a gene of interest. The DNA, polypeptide and the methods may be used for inhibiting or delaying cell death. The current sequence is that of the Chinese hamster anti-apoptosis bcl.xL-related PCR primer which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing or preventing death of T cells by bcl-XL protein regulation used to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases.
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                                                                                                                                      Sequence 37 BP; 9 A; 12 C; 10 G; 6 T; 0 U; 0 Other;
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95US-00481739.
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07-JUN-1995;
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°, 0; Gaps Query Match 100.0%; Score 20; DB 2; Length 39; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 20; Conservative 0; Mismatches 0; Indels

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GenCore version 5 Copyright (c) 1993 - 2005 C	nucleic search, using sw model February 4, 2005, 20:41:45; (wi	US-09-753-169A-2 20 1 tcccggttgctctgagacat 20 IDENTITY_NUC Gapop 10.0 , Gapext 1.0	s, 18219865908	length length	.ng: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	EST:* 1: gb_estl:* 2: gb_est2:* 3: gb_htc:* 4: gb_est4:* 5: gb_est4:* 6: gb_est6:* 7: gb_est6:* 9: gb_est5:* 9: gb_est5:*	of [ga]	SUMMARIES Query Match Length DB ID	1	100.0 252 2 100.0 262 4 100.0 275 4 100.0 297 2 100.0 301 4
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20 100.0 3250 20 100.0 3250 20 100.0 3250 20 100.0 3270 20 100.0 3370 20 100.0 3481 20 100.0 3481 20 100.0 3570 20		BE796096 BE796096 BE796096 BE796096 BE796096 BE796096 BE796096 BE796096 BE796096 BER76096 I GI:10217294 BENT. Homo sapiens Rukaryota, Metazoa, Chordata, C Mammalia, Eutheria, Primates; C Mammalia, Eutheria, Primates; C Mammalia, Futheria, Primates; C Manmalia, Futheria, Primates; C Mational Institutes of Health, Unpublished (1999) Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dorn/DTP CON Library Preparation: Ling Clone distribution: MGC clone found through the I.M.A.G.B. Co Plate: LLCM802 row: d column: High quality sequence start: 25 Corganism="Mona" (Colone" Inne="Mona" (Alone="Mona") (Alone="Mona") (Alone="Mona") (Alone="Mona") (Alone="Mona") (Alone="Mona") (Alone "Mona") (Alone "Mona")	(Stratagene)
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Homo sapiens (human)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 129)

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM135 row: k column: 02
High quality sequence stop: 129.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                       Gaps
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Query Match
100.0%; Score 20; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 29;
Matchés 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mus musculus
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Best Local Similarity
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CG608749.1
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KEYWORDS
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ORGANISM
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BE275197/c
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CG608749/c
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AUTHORS
TITLE
JOURNAL
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Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.

Location/Qualifiers
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                                                                                                   Lambrowicz B.P. Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.P.
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fiddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-O., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Saparks, M.J., Van Sligenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, O., Person, C. and Sands, A.T.
Whkl kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 136)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
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    .136
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"

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Tissue Procurement: ATCC/DCTD/DTP
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/clone="OST289185"
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/db_xref="taxon:9606"
/clone="IMAGE:3614708"
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BF688810 177 bp mRNA linear EST 22-DEC-2000 602184995F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299479 5',
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200)
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Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
plate: LiCMA156 row: n column: 24
High quality sequence start: 2
High quality sequence stop: 177.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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/organism="Homo sapiens"
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       114 TCCCGGTTGCTCTGAGACAT
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Matches 20;
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KEYWORDS
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BF688810/c
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DEFINITION
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TITLE
JOURNAL
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/tissue_type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NHH MGC_20"
/clone_lib="NHH MGC_20"
/note="Organ: sKin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GCACAGGG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/clone_lib="NIH_MGC_43"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5;
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACAGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
Callifornia, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lll.gov
thtp://mage.lll.gov
thtp://mage.lll.gov
High quality sequence stop: 162.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 2; Length 151; 100.0%; Pred. No. 30; ive 0; Mismatches 0; Indels
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'db_xref="taxon:9606"
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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(LLNL)

RESULT 5 BM050693/c DEFINITION

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LOCUS

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE AUTHORS TITLE JOURNAL COMMENT

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Gaps

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REFERENCE

1 TCCCGGTTGCTCTGAGACAT 20

ORIGIN

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issue_type="melanotic melanoma"
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BG478819
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BG478819/c
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Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nat. Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
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1. (bases 1 to 210)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="infant"
/clone_lib="Infant_brain"
/note="organ: brain; Vector: lafmid BA; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1294 row: 1 column: 21
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                                                                                                                                                                                    The Institute for Genomic Research 7712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                /mol type="mRNA"
/db xref="ATCC (inhost):151593"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4578596"
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                                                                                                                                                Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                           Other ESTs: THC105965
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BG334446/c
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/tissue_trype="melanotic melanoma"
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/lab host="bH10B (phage-resistant)"
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/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
CoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size_1:8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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602525369F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643800 5',
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ArCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov

Plate: LLCM1414 row: i column: 17

High quality sequence stop: 213.

Location/Qualifiers
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/lab host="DHIOB (phage resistant)"
/clone lib="NIH MGC_20"
/note="Organ: skin; Vector: pOTB); Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/KhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 213)
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/clone="IMAGE:4643800"
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RESULT 10 BG752203/c LOCUS

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DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

FEATURES

REFERENCE

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cloned into EcoRI/Khol sites using the following 5'
adaptor: GGCACGG(G). Size-selected >SODD for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 225)
                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at: image.llnl.gov
Plate: LLCM504 row: f column: 17
High quality sequence start: 38
High quality sequence stop: 223.
Location/Qualifiers
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
      National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Thasue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 2; Length 223; 100.0%; Pred. No. 32; cive 0; Mismatches 0; Indels
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                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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High quality sequence stop: 225.
Location/Qualifiers
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/mol type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 20; Conserv
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BF026532/c
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/tissue type="normal pigmented retinal epithelium"
/lab.host="BilloB (phage-resistant)"
/clone lib="WIH MGC 43"
/clone lib="WIH MGC 43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sing using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
                                                                                                                                                                                BG752203 218 bp mRNA linear EST 15-MAY-2001
602731335F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4874865 5',
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 218)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 223)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1755 row: e column: 10
High quality sequence stop: 218.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
165 TCCCGGTTGCTCTGAGACAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 TCCCGGTTGCTCTGAGACAT 151
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BE727284
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

BE727284/c DEFINITION

LOCUS

RESULT 11

ORIGIN

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Gaps

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/tissue_type="leiomyosarcoma cell line"
/lab_host="BHIOB (phage-resistant)"
/clone_lib="NHH MGC_46"
/clone_lib="NHH MGC_46"
/clone_lib="NHH MGC_46"
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using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                              BF685843 22-DEC-2000 02143136F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304288 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1169 row: g column: 09
High quality sequence stop: 230.
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
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100.0%; Pred. No. 32;
tive 0; Mismatches
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/clone="IMAGE:4304288"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 rcccccrrccrcrcacacar 163
     1 TCCCGGTTGCTCTGAGACAT 20
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BG746689
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nes 20; Conserv
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BG746689/c
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BF685843/c
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Matches
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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/Lissue type="melanotic melanoma"
/Lissue type="melanotic melanoma"
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/Lissue type="melanoma"
/Lissue Lorgan: Bin; Vector: pOTB7; Site 1: XhoI; Site 2:
BCORI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACAGG(G). Size-selected >SOODp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE275637 227 bp mRNA linear BST 13-JUL-2000
601121162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988806 5',
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                                             /lab host="DH10B (phage-resistant)"
/clone lib="NHH MGC 20"
/clone lib="NHH MGC 20"
/clone lib="NHH MGC 20"
/clone lib="NHH MGC 20"
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1 (bases 1 to 227)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: egapbs-rémail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The I.M. A.G.B. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov Plate: LLCWPB row: k column: 15
High quality sequence start: 27
High quality sequence stop: 227.

Location/Qualifiers
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                          /tissue_type="melanotic melanoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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clone="IMAGE:3955413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE275637.1 GI:9150595
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Gaps

us-09-753-169a-2.rst

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/done=TWAGE:4857171"

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/lab.host="BH10B (phage-resistant)"

/clone_lib="WIH MGC 15"

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/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:

BOOKI; cDNA made by oligo-dr priming. Directionally

cloned into EcoRIXAtol sites using the following 5;

adaptor: GGCACGAG(G). Site-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)"
      E 1 (Dases 1 to 232)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-ramil: nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMT709 row: d column: 04

High quality sequence stop: 232.

High quality sequence stop: 232.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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CQ138575 Sequence
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Patent: JP 2002519048-A 3 02-ULL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
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ANTISENSE OLIGONUCLEOTIDE
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefe"taxon:32630"
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CQ112670 Sequence
CQ18528S Sequence
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CQ732731 Sequence
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S78284 bcl-xshort=
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0210449-A 13216 07-FEB-2002;
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Patent: JP 2002519048-A 18 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PD 02-JUL-2002
PP 02-JUL-2009 JP 2000557839
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Patent: JP 2002519048-A 17 02-JUL-2002;
Patent: GC CCLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/17
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                         Oligonucleotide inhibitors of bcl-xL.
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Oligonucleotide inhibitors of bcl-xL.
BD235166 101:33044936
JP 2002519048-A/18.
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misc_binding (8)...(9)
misc_binding (13)...(15)
misc_binding (17)...(20).
Location/Qualifiers
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02-JUL-1999 JP 2000557839
02-JUL-1998 US 09/10961
CY A STEIN
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JP 2002519048-A/17.
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artificial sequences.
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Stein, C.A.
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synthetic construct
artificial sequences.
1 (bases 1 to 20)
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20; Conservative
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PAT 21-JAN-2004

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/note="MAP TO ALILY 00781.9~EXPRESSED IN HEART, SIGNAL = 1.6-SWISSPROT HTT: Q07817, EVALUE 2.00e-18~EST HUMAN HTT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE 1.00e-65"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENONE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130-PB 0004 WO 3<br/>
3<br/>
4.150-US 60/180, 312-R151- 04 February 2000 (04.02.00)<br/>
4.150-US 60/180, 312-L15-04 February 2000 (04.02.00)<br/>
4.150-US 60/180, 312-L15-04 February 2000 (04.02.00)<br/>
4.150-US 60/180, 312-L15-04 February 2000 (04.02.00)<br/>
4.150-US 60/180, 312-15-04 GB 24263.66-151-03<br/>
4.150-US 60/180, 312-15-04 GB 24263.66-151-03<br/>
4.150-US 60/180, 312-15-04 GB 74-151-15-05<br/>
4.150-US 60/180, 408-151-15-05<br/>
4.150-US 60/180, 408-151-15-05<br/>
Molecular Dynamics Sequence Listing Engine Patent: WO 0157273-A 21759 09-AUG-2001;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
patent: WO 0157274-A 16681 09-AUG-2001;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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llarity 100.0%; Pred. No. 32;
Conservative 0; Mismatches 0
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              100.0%; Score 20; DB
100.0%; Pred. No. 32;
tive 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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                   Query Match
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/db_xref="taxon:9666"
/nofe="wap TO ALIT:381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 5.5-GMISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT: AM820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE 1.00e-65"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 21529 09-AUG-2001,
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 21565 09-AUG-2001,
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Sequence 21529 from Patent WO0157272.
CQ112670
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'db xref="taxon:9606"
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Pred. No.
                Pred. No.
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100.0%; Pr
tive 0;
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CQ151543.1 GI:41158893
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CQ112670
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
2.2-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT:
AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
1.00e-65"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organia="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/mote="mAP TO AL117381.9-EXPRESSED IN BRAIN, SIGNAL = 2~SWISSPROT HIT: Q07817, EVALUE 2.00e-18~EST HUMAN HIT: AW820481.1, EVALUE 1.00e-65~NT HIT: Z23115.1, EVALUE
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                                                                                                                                                                                Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                    linear
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PE Corporation (NY) (US)
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CQ732731
                                                                                                                                                                                Score 20; DB 6
Pred. No. 32;
); Mismatches
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      'organism="Homo sapiens"
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CQ346752.1 GI:41295823
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ses 20; Conserv
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Locus
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CQ346752
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/mol type="unassigned DNA"
/db xref=taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN FETAL LIVER, SIGNAL
-4.1-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
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/db Aref="taxon:9606"
/note="MAP TO ALI17381-9-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820491.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung
Patent: WO 0186003-A 21250 15-NOV-2001;
Aeomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human fetal liver
Patent: WO 0157277-A 20737 09-AUG-2001;
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PAT 03-FEB-2004

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Rattus norvegicus bcl-x short mRNA, complete cds.
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AF279286/c
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Behrens,T.W.
Direct Submission
Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein id="MAA82172.1"
/db xref="d1:50646"
/translation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEFTBAE
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RAFSDLSQLHITPGTAYQSFEQDTFVDLYGNNAAAESRKGQERFNRWFLTGWTVAGV
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Mus musculus bcl-x short (bcl-x long) mRNA, complete cds.
U10100
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 513)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fang, W., Rivard, J.J., Mueller, D.L. and Behrens, T.W. Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xrefe"taxon:10090"
/db_ill="MEHL 555.1 RNA"
/note="alternatively spliced transcript of bcl-x long,
                                                                                                                                         Gaps
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                                                                                                          Length 387;
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                                                                                                         100.0%; Score 20; DB
ilarity 100.0%; Pred. No. 30;
Conservative 0; Mismatches
              1. .387
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/organism="Mus musculus"
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 Location/Qualifiers
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/gene="bcl-x long"
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                                                                                                                                                                                     347 GCCACAGTCATGCCCGTCAG 328
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Best Local Similarity 100.
Matches 20; Conservative
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Matches 20; Conserva
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AF136230/c
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                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                         KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
FEATURES
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                                                                           ORIGIN
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RETPSAINGNPSWHLADSPEVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
RAFSDLTSQLHITPCTAYQSFEQDSFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGV
VLLGSLFSRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear ROD 02-JUL-2000 complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'translation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEFTEPE"
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Direct Submission
Submitted (16-UIN-2000) Neurology, University of Pittsburgh, 3500
Terrace Street, Pittsburgh, PA 15261, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                               University of Pittsburgh, 3500
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0
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                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Spraque-Dawley"
/db_rref="taxon:10116"
/tissue_type="brain"
/note="Isolated from an ischemic brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 513)
Cao, G., Chen, J. and Chen, D.
Bol-Xs. expression and its role in brain ischemia
                                                                                                                                                       Tobases 1 to 513)

He,X.J., Jin,K.L., Graham,S.H. and Simon,R.P. Direct Submission
Submitted (22-Mar.1999) Neurology, University Terrace Street, Pittsburgh, PA 15213, USA
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Rattus norvegicus bcl-x short form mRNA,
AF279286
                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
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1. .513
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10116"
/tissue_type="cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="AAD33683.1"
/db_xref="G1:4928688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              l. .513
/codon_start=1
/product="bcl-x_short"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
                                             Rattus norvegicus (Norway rat)
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- Chen, J. and Chen, D.
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100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0;
AF136230.1 GI:4928687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF279286.1 GI:8896160
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/product="bcl-x short form"
/protein_id="AAR81261."
/db_xref="G1:8896161"
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RETPSAINGNPSWHLADSPANNGATCHSSSLDAREVIPMAAVKQALGEAGDBFELRYR
RAFSDLTSQLHITPGTAXQSFEQDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGV
VLLGSLFSRK"
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Query Match 100.0%; Score 20; DB 10; Length 513; Best Local Similarity 100.0%; Pred. No. 29; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

ORIGIN

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8 8

Search completed: February 4, 2005, 23:30:38 Job time : 482.738 secs

	Ltd.
5.1.6	Compugen
version	- 2005
GenCore	(c) 1993
	Copyright

OM nucleic - nucleic search, using sw model

February 4, 2005, 15:50:53; Search time 258.033 Seconds (without alignments)
406.880 Million cell updates/sec Run on:

US-09-753-169A-3 20 Title: Perfect score:

1 gccacagtcatgcccgtcag 20 Sequence:

IDENTITY NUC Gapox 1.0 Scoring table:

4134886 segs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04: geneseqn2001as: geneseqn1990s:* geneseqn2002bs: geneseqn2001bs: geneseqn2002as: genesegn2003as Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs geneseqn2003ds geneseqn20048:

geneseqn2003bs

STRAMMIN

Abs33819 Human liv Abs08825 Human gen Ach70569 Human gen Ach70569 Human gen Ach52636 Chinese h Ach52636 Chinese h Ach52640 Chinese h Ach52640 Chinese h Ach43464 cDNA clon Ach43646 cDNA clon Ach45994 Human apo Ach45994 Human apo Ach59159 Human cDN Ach583150 Toxicolog Ach313132 Human cDN Ach58350 Human cDN Ach58350 Human cDN Ach58350 Human cDN Ach686364 Bclx gen Ach40079 Bclx gen Ach40079 Bclx gen Ach593644 Bclx gen	
ABS33839 ABS08825 ABS08825 ADH50569 ADH52636 ADH52638 2 ADH52640 ADH43464 2 ADM55994 AAQ81699 AAQ81699 AAT407079 AAQ81698 AAT40079 AAQ81698 AAT40079	AAC90810 ABK84766 ABK8476641 O ADDS6779 O AAD54187 1 AD132104
4 9 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	44081111
5887 5887 7402 7402 7437 7437 7437 7437 7437 7437 7437 743	000000000000000000000000000000000000000
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0 0 0 0 0 0 0 0 0 0 0 0 0 0	0000000

ALIGNMENTS

Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Bcl-Xl mRNA specific antisense oligo C. (UYCO) UNIV COLUMBIA NEW YORK. AAZ46973 standard; DNA; 20 BP. 98US-00109614. 99WO-US015250. 14-APR-2000 (first entry) WO200001393-A2. Homo sapiens. 02-JUL-1999; 02-JUL-1998; 13-JAN-2000. AAZ46973; RESULT 1 AAZ46973

Stein CA;

WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bel-XL, useful for reducing bel-XL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

which reduce or eliminate expression of the anti-apoptotic protein belax. The oligonucleotides can be introduced into tumour cells to reduce belax. production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bel-2 family proteins (to which bel-xi belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bel-xi production to promote the regression of vascular The invention provides antisense oligonucleotides or their derivatives

RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method of the invention.

Sequence 25 BP; 3 A; 7 C; 9 G; 6 T; 0 U; 0 Other;

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DB 12; Length 25;

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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpyridyl) porphine and/or tetra meso- (anilinium) porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-Xl mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
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                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                   Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                   1 GCCACAGTCATGCCCGTCAG 20
                                                                                                                                                                                                                                                                                                                                                         BP.
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Matches 20; Conservative 0
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BURCZYNSKI M E.
TREPICCHIO W L.
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(BURC/)
(TREP/)
(DORN/)
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ID ADP1.

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                                                                                                                                                                                                                                                                                                                     ss; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood monounclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from non-blood disease such as solid tumor. The solid tumor is chosen from peripheral blood sample comprises enriched PBMCs. The peripheral blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples genes that are differentially expressed in peripheral blood samples is a whole blood sample of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a probe to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dorner A, Stover JA;
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                                                                                                                                                                                                                                                                                         Renal cell carcinoma differentially expressed gene probe #3709.
                                    0; Indels
100.0%; Score 20; DB 12
100.0%; Pred. No. 5.7;
iive 0; Mismatches
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                                                                    1 GCCACAGTCATGCCCGTCAG 20
                                                                                                    GCCACAGTCATGCCCGTCAG 4
                                                                                                                                                                                        BP.
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03-APR-2003; 2003US-0459782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-2003; 2003WO-US037481
                                                                                                                                                                                      ADP17304 standard; DNA; 25
                                                                                                                                                                                                                                                         26-AUG-2004 (first entry)
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                                   20; Conservative
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TREPICCHIO W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-460799/43.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DORNER A.
STOVER J A.
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TWINE N C.
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Sloni DK;
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                                   Matches
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ADP17304/
                                                                                                                                                     RESULT
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The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood monounclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample comprises enriched pends is useful for identifying genes that are differentially expressed in peripheral blood samples isolated at different stages of progression, development or treatment of

Disclosure, SEQ ID NO 1711; 350pp; English.

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detect a gene that is differentially expressed and detected by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental specific genes, and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human spliced transcript detection oligonucleotide SEQ ID NO:13216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant; transcriptome; oligonucleotide library; ss.
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                                                                                             100.0%; Score 20; DB 12; Length 25; 100.0%; Pred. No. 5.7;
                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Faigler S;
                                                      Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;
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                                                                                                                                     0; Mismatches
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                                                                                                                                                                           1 GCCACAGTCATGCCCGTCAG 20
                                                                                                                                                                                                    22 GCCACAGTCATGCCCGTCAG 3
                                                                                                                                                                                                                                                                                                                    ABN40468 standard; DNA; 60 BP
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                   20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-257383/30.
                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          ABN40468;
                                                                                             Query Match
                                                                                                                    Best Loca
Matches
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ABN40468/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                          88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe;
                                                                                    Gaps
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directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 20737; 639pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #20737.
                                                                                    0; Indels
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                                                          6; Length
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                             Sequence 60 BP; 6 A; 18 C; 20 G; 16 T; 0 U; 0 Other;
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0
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100.0%; Pred. No. v...
                                                       Score 20; DB
Pred. No. 6.2;
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                                                                                                                                     36 GCCACAGTCATGCCCGTCAG 17
                                                                                                                 GCCACAGTCATGCCCGTCAG 20
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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Best Local Similarity 100.0%;
Marches 20; Conservative
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2000US-0207456P.
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                                                     Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                               (first entry)
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27-SEP-2000;
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed single exon probe SEQ ID NO: 21565.
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID NO 16681; 530pp; English.
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                         2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                   30-JAN-2001; 2001WO-US000666
                                                                                        2000US-0180312P
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27-SEP-2000; 2000US-0236359P
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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30-JUN-2000;
03-AUG-2000;
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               09-AUG-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                          Probe #21529 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #16681 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                           Probe; microarray; human; placenta; antenatal diagnosis
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1 Similarity 100.0%;
20; Conservative 0.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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               DNA; 127
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                                                                                        (first entry)
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                                                                                                                                                                                genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG, Hanzel DK,
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             AAI52843 standard;
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Best Local &
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present invention provides a number of single exon nucleic acid
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Matches
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                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                     duman genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                        Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                              Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
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                                                          Rank DR
                                                                                                                  gene expression in human bone marrow.
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                                 (MOLE-) MOLECULAR DYNAMICS INC
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                                                        Chen W,
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27-SEP-2000; 2000US-0236359P.
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2000US-0234687P.
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                                                        Hanzel DK,
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                                                                               WPI; 2001-488900/53
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Best Local Similarity
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
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Example 4; SEQ ID NO 20846; 650pp + Sequence Listing; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liver, comprising one of 13109 defined nucleotide sequences given in the stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe (SENP) (1) for
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring human gene expression in a sample derived from human adult
                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, single exon nucleic acid probe, liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
                                                                                                                                                                             Length 127;
                                                                                                                                                                                                               Indels
                                                                                                                                       Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                               ö
                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human liver single exon probe, SEQ ID No 21759
                                                                                                                                                                                              6.7;
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                           Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 21759; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                   1 GCCACAGTCATGCCCGTCAG 20
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                                                                                                                                                                                                                                                                                                                                                                             ABS46769 standard; DNA; 127 BP
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                                                                                                                                                                                                                                                                         GCCACAGTCATGCCCGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                             100.08;
                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0207456P
2000US-00608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                            Local Similarity 100.
1es 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488898/53
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ACH84269/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes it he novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a enkaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of
                                                                                                                                                                                                                                                                                                  Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spatially-addressable set of single exon nucleic acid probes, used to
                                                                               Gaps
                                                                                                                                                                                                                                                                           Human genome-derived single exon probe ORF from lung SEQ ID No 21250
                                                                            ;
0
                                                 100.0%; Score 20; DB 4; Length 127; 100.0%; Pred. No. 6.7; tive 0; Mismatches 0; Indels
                         Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 21250; 634pp; English.
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR
                                                                                                                   30 GCCACAGTCATGCCCGTCAG 49
                                                                                                      1 GCCACAGTCATGCCCGTCAG 20
                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-0207456P
30-JUN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                             ABS21259 standard; DNA; 127
                                                                                                                                                                                                                                                  (first entry)
                                                              Local Similarity 100.
tes 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                  19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-NOV-2001
                                                                                                                                                                                                                        ABS21259;
                                                     Query Match
                                                                             Matches
                                                                                                                                                                      RESULT 11
                                                                                                                                                                                    ABS21259
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the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising the expression of each of the exons in the tissues and/or cell types indicates that the expression of each of the exons should be assigned to a single gene; a peptide comprising one compression of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the composition of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the composition of the study of lung diseases such as asthma, lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPP), interstitial lung diseases (LDP), familial idiopathic pulmonary fibrosis, pulmonary controlled in proteinosis, pulmonary avocatance is a single exon probe open reading frame of the controlled in sequence data for this patent did not form part of invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at fip. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 6; Length 127; 100.0%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome derived single exon probe #17464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCCACAGTCATGCCCGTCAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACH84269 standard; DNA; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 100.
Matches 20; Conservative
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003194704-A1.
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide concorning at least 8 amino acids of any of the 6888 amino acid sequences in the specification. The probe is a single exon probe that cencoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that bybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially.

Comprises of single exon nucleic acid probes for measuring human cells each of single exon nucleic acid plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a method of contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), and a contiguous amino acids of selling and/or licenshing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing to measure gene expression, a method of providing contains a database having a plurality of records (est record including data by subscription, and a computer-readable cated bove. The probes may be used as tools for surveying tissues to detect the presence of expressed and apparatus are useful in gene capecific exon, or in constructing genome-derived single exon probe of the printing gene expressing the Operance of a preming alterations in the genomic locate that includes their sequence as a human capelle exon probe of the printed specification, and express segdata.uspto.gov/sequence.html?DocID=20030194704 Claim 1; SEQ ID NO 17464; 80pp; English. electronic format directly

Sequence 179 BP; 37 A; 53 C; 48 G; 41 T; 0 U; 0 Other;

100.0%; Score 20; DB 12; Length 179; 100.0%; Pred. No. 6.9; 0; Indels 0; Mismatches 20; Conservative Query Match Best Local Similarity Matches 20; Conserv ò

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Gaps

; 0

1 GCCACAGTCATGCCCGTCAG 20 118 GCCACAGTCATGCCCGTCAG 99 셤

503/c ACD94503 standard; cDNA; 299 BP. 23-SEP-2003 ACD94503; RESULT 13

Human colon cancer cell expressed cDNA #2915. (first entry)

agriculture, food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; Open reading frame detection; genome sequencing; colon cancer; breast cancer; population genome analysis; genetic shift; cancer; antibiotic registance; antibiotic non-tolerance; congenital disease; gene; ss.

Homo sapiens.

US2002155438-A1.

24-OCT-2002

99US-00406117. 27-SEP-1999;

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nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a contig, all or part of a genome of an organism; and for sequencing all or part of a genome of an organism. mRNA is obtained from mammalian or human cell which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of populations of subjects and can be used to carry out genetic analyses of large or small populations. Further, it can be used to study living systems to determine if, e.g. there have been genetic shifts which render an individual or population more or less likely to be afflicted with colerance, and so forth. The method can also be used in the study of congenital diseases, and the risk of affliction to a foetus, as well as through ove or sperm. The analyses for pathological conditions can be carried out in all animals, plants, birds, fish, etc. Using this method, the area of agriculture, for example the genomes of food crops can be arried out in all animals, plants, birds, fish, etc. Using this method, this hards of agriculture, for example the genomes of food crops can be arried on the study of the organization of agriculture, for example the genomes of food crops can be arried on the study of the organization of agriculture, for example the genomes of food crops can be arried on the study of the organization of a definition of the organization of the organization of a definition of the organization of a definition of the organization of the organization of a definition of the organization of a definition of the organization of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (I), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting nucleic acids. The method is useful for: determining that a known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     studied to determine if resistance genes are present, defects in plant genomes can also be studied in this way. Similarly, the method permits determination of the pathogens which integrate into the genome, such as retroviruses and other integrating viruses such as influenza virus, have undergone shifts or mutations, which may require different approaches to therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially
                                                                                                                                                                                                                                                                                                                                                                     an organism e.g. a human
oligonucleotide primer at
                                                                                                                                                                                                                                                                                                                                                              Determining open reading frames of genome of an organism e.g. a suffering from cancer involves use of single oligonucleotide proom stringency for preparing single-stranded cDNA from mRNA of
                                                                                                                                                                                                                                  Brentani RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Page 432; 959pp; English.
                               98US-00196716.
                                                                                                                                                                                                                               Simpson AJG, Neto ED,
                                                                                               SIMPSON A J G.
                                                                                                                                   NETO E D.
BRENTANI R R.
                                                                                                                                                                                                                                                                                               WPI; 2003-182626/18.
                               20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Individual
                                                                                                                                   (NETO/)
(BREN/)
                                                                                               (SIMP/)
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Gaps ö Score 20; DB 10; Length 299; Pred. No. 7.3; 0; Indels 100.0%; Scc... 100.0%; Pred. No. '... 1 GCCACAGTCATGCCCGTCAG 20 GCCACAGTCATGCCCGTCAG 77 ADK66037 standard; DNA; 337 BP. Best Local Similarity 100.0 Matches 20; Conservative 06-MAY-2004 (first entry) ADK66037; Query Match ADK66037/c RESULT 14 8 셤 0×2×5×8×

Standardized polynucleotide system polynucleotide #8.

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eliminates sequencing of non-coding portions. This sequence repres polynucleotide isolated from human colon cancer cell CDNA library

Sequence 299 BP; 64 A; 95 C; 74 G; 66 T; 0 U; 0 Other;

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The present invention relates to a standardized polynucleotide system, which comprises at least one carrier nucleic acid, at least 3 bigonucleotides, as primers and target-specific, fluorescently labeled probe and optionally at least one set of stabilized controls (standard RNA or DNA) of known concentration and instructions. The system comprises any of 20 sets of one control, two primers and one target-specific probe. The standardized polynucleotide system can be used for quantitative, real-time detection of target nucleic acids, especially analysis of genes or gene products, e.g. for individualized medical diagnosis, in veterinary medicine, functional genomics, clinical pharmacology, pharmacogenetics, pharmacoeutical testing, analysis of food or environmental samples and also for ultra-sensitive detection of proteins by immuno-PCR. The present sequence is a polynucleotide used in the system of the invention.
ss; standardized polynucleotide system; medical diagnosis;
functional genomics; sample analysis; pharmacogenomics; sample analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                 Standardized polynucleotide system, useful for quantitative, real-time determination of nucleic acid, comprises stabilized standards, primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 7; 38pp; German.
                                                                                                                                                                                              28-FEB-2002; 2002DE-01009071
                                                                                                                                                                                                                                         28-FEB-2002; 2002DE-01009071
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-732912/70.
                                                                                                                                                                                                                                                                                                                           Koehler T, Rost A;
                                                                                                          DE10209071-A1
                                                               Unidentified
                                                                                                                                                     25-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and probe
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                               Gaps
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; Score 20; DB 10; Length 337; ; Pred. No. 7.4; 0; Mismatches 0; Indels C
     100.0%;
100.0%;
                           20; Conservative
                 Best Local Similarity
     Query Match
                              Matches
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259 GCCACAGTCATGCCCGTCAG 240 1 GCCACAGTCATGCCCGTCAG 20 ð

Search completed: February 4, 2005, 21:52:40 Job time: 261.033 secs

ACH46093 standard; cDNA; 492 BP ACH46093;

(first entry) 13-OCT-2003 Human infant brain cDNA #156

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

Homo sapiens

US2003073623-A1

17-APR-2003

30-JUL-2001; 2001US-00918995

30-JUL-2001; 2001US-00918995

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polyneptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences or ensured in assessing biolynucleotide. The nucleic acid sequences or ensured in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations cappoints in a sequence and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense bNA or RNA. The purified polypeptide is useful for generating antisense bNA or RNA. The purified polypeptide is useful for generating antisense bNA or RNA. The purified polypeptide is useful for generating antisense bNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence date of the interval of the printed specification, but was
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                                                                                                                                    Dickson MC,
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    DRMANAC R T.
                                                                 DICKSON M C.
JONES L W.
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BIO51278
BM741875
AA903741
AA903741
BM818387
AC159206
AC1

OM nucleic

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Sequence:

Searched:

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Database

Result Š.

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 119)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRI&t2=MRI-HT1067-011200-001-a10&t3=2000-12-01&t4=1)

Seq primer: puc 18 forward
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...
/mol_type="mRNA"
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Site_2: Smal; A mini-library was made by cloning products
                                                                                                                                                                                                                                                                                                                                         BF840557
MRL-HT1067-011200-001-a10 HT1067 Homo sapiens CDNA, mRNA sequence.
BF840557
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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High quality sequence stop: 119.
Location/Qualifiers
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BE378810
CG604974
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BM741875
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AA823283
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CG659215 OST436826
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                                                                               20:41:45; Search time 2384.67 Seconds. (without alignments) 305.616 Million cell updates/sec
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           5.1.6
Compugen Ltd.
                                                                                                                                                                                                                    32822875 seqs, 18219865908 residues
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           GenCore version
Copyright (c) 1993 - 2005
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CG632613 OST351228 CG559660 OST178957 CG663330 OST448394

CG559660 CG663330

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EST 13-JAN-2001

OST378118 OST391582

OST287334

OST329865

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BF948716.1 GI:12365991
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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db xref="taxon:9606"
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/note="Organ: head neck; Vector: pucl8; Site 1: Sml1;
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derived from ORBSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUCl8 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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Fax: +55-11-2707001
Email: asimpson@ludwig.org_br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-HT0380-
010200-101-f0&&t3=2000-02-01&t4=1)
Seq_primer: puc 18 forward
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                     Gaps
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HCGP http://www.ludwig.org.br/ORESTES.
The FAPESF/LICR Human Cancer Genome Project Unpublished (1999)
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High quality sequence stop: 133.
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/mol_Lype="mrm" or provided by the control of the c
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1 (bases 1 to 140)

Bias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NN1152-311000-454-b02&t3=2000-10-31&t4=1)
Seq primer: puc 18 forward: 31
High quality sequence start: 31
High quality sequence stop: 140.
Location/Qualifiers
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1 (bases 1 to 167)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
CM2-NN1152-311000-454-b02 NN1152 Homo sapiens cDNA, mRNA sequence
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shorgun sequencing of the human transcriptome with ORF expressed
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/organism="Homo sapiens"
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Homo sapiens (human)
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Best Local Similarity 100.0
Matches 20; Conservative
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MEDLINE
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AUTHORS
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S Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Pigott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T. Wnkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_tree="manage: "mol_tree="manage: "mol_tree="manage: "mol_tree="manage: "mol_tree="manage: "mol_tree="moltree" |
/db_xstef="taxon:9606" |
/db_stage="manage: "moltree="moltree" |
/dougan: nervous tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from (PRESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of profiles into the pUC18 vector. Reverse transcription of prissue mRNA and CDNA amplification were performed under low stringency conditions."
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O.,Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0202-
081200-298-D05&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 167.
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                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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OST379295 Mus musculus 129Sv/Ev Mus musculus genomic clone
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20202663
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AUTHORS
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 194)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva, W. Dr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deolivaira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0175-011200-514-a04&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 194.
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                                                                                       Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.
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QV3-ET0175-011200-514-a04 ET0175 Homo sapiens CDNA, mRNA seguence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/do_stage="Adult"
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/note="Organ: lung_tumor; Vector: puc18; Site_1: Smal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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/db_xref="taxon:10090"
/clone="0ST379295"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1298v/Ev"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                     1. .177.
/organism="Mus musculus"
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/organism="Homo sapiens"
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AI904167/c
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CG656719/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 216)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-091100-004-bl0&t3=2000-11-09&t4=1)
Seq primer: puc. 18 forward
High quality sequence start: 25
High quality sequence stop: 216.
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mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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PM2-CI0111-091100-004-b10 CI0111 Homo sapiens CDNA,
BF806802
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100.0%; Pred. No. 50;
ive 0; Mismatches
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VERSION
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PUBMED
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SOURCE
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BF806802
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DB 2; Length 216;

Score 20; DB Pred. No. 50;

100.0%;

Query Match Best Local Similarity

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1 (bases 1 to 233)
Dias Neto,E., Garcia,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
                                                                                                                                                                                                       GSS 02-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lambrowicz, B. Y. Abuin, A., Ramirez-Solis, R., Richter, L.J., Pinch, R.A., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Priddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markeelch, D., Pance, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T. Whkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
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/clone_lib="Mus musculus 129Sv/Ev"
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/mol_type="genomic DNA"
/strain="129Sv/Ev"
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Pred. No.
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/clone="OST429779"
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                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
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1 GCCACAGTCATGCCCGTCAG 20
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AI904167.1 GI:6494554
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Best Local Similarity 100.
Matches 20; Conservative
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Homo sapiens
                                                                                                                                         source
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Eukaryota; Matezoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Bases 1 to 253)
Sambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnkl Kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Droc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html
&t3=090299&t4=1)
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Brd43"
//clone_lib="Grgan: breast; Vector: puc18; Site_1: Sma1; Site_2: Sma1, A min-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                        \operatorname{Simpson}, A \ldotp J . Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG659215 253 bp DNA linear GSS 02-OST436826 Mus musculus 129Sv/Ev Mus musculus genomic clone OST436826, genomic survey sequence.
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0
                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lexicon Genetics Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: puc 18 forward
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="female"
                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
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CG659215/c
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KEYWORDS
SOURCE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                               TITLE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

I (basea 1 to 254)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J. Fine, L.D., FitzGarald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Kalley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Fellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Nuysen, D.T., Raldeman, J.F., Li, Y., Bednarik, D.P., Feng, P., Ferrie, A., Gruber, C.J., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Maissner, P.S., Olsen, H., Raseltion, Wei, Y.-F., Wing, J., Ku, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of CDNA Sequence
4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.

Location/Qualifiers
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T28063 254 bp mRNA linear EST 06-SEP-
EST26052 Human Brain Homo sapiens cDNA 5' end similar to bcl-x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="embryonic stem cell"
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699955
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                   organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No
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T28063
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Best Local Similarity 100.0
Matches 20; Conservative
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20

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sequence tags
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                                                                                                                                                                                                                  AW820481
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                                                                                                                                                                                            DEFINITION
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/clone_lib="R1055"
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Parent application
No. 196,716 - ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue_mRNA and cDNA amplification were performed under
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                                                                                                                                                                                                                                                                                                                                                                                                         BF823588 13-JAN-2001 RCS-RT0055-221200-011-G02 RT0055 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-270701

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-21200-011-G02&t2=22000-12-22&t4=1)

Seg primer: puc 18 forward

High quality sequence stop: 283.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                  Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                 100.0%; Score 20; DB
100.0%; Pred. No. 51;
ive 0; Mismatches
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Location/Qualifiers
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BF823588.1 GI:12164528
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                                                                                                                                                                                                             20; Conservative
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VERSION
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PUBMED
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BF823588
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SOURCE
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0; Gaps

Query Match
100.0%; Score 20; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 0; Indels

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/note="Torgan: stomach; Vector: pucl8; Site_1: Smal;
/note="Torgan: stomach; Vector: was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application of 196,716 - Ludwig Institute for Cancer Research)
profiles into the pucl8 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-140
Seq primer: puc 18 forward
                                                                                                                                                                                                      AW820481 332 bp mRNA linear EST 17-MAY-2000 QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Garvalho, A.F., Matsukma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 332)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. B. (bases 1 to 337)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payre, R., Potter, D.G., Qian, N., Sahwi, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
Whkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Processing Company (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
mail: materials@elexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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2 Cambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, B.C., Edwards, J., Finch, R.A.,
Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Rey, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Olann, V., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Shu, Q., Person, C. and Sands, A.T.
What kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
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/clone_lib="Mus musculus 129Sv/Ev"
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/strain="129Sv/Ev"
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                Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9,392(6676):608-11) Class: Gene Trap.
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                                                                                                                                  /mol_type="genomic DNA"
/strain="1295v/Ev"
/db_xref="taxon:10090"
/clone="OST222203"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
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Pred. No. 53;
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Job time : 2390.67 secs
                                                                                                                  /organism="Mus musculus'
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Email: materials@lexgen.com
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BT001208 Homo sapi BT001248 Synthetic U72398 Human Bcl-x AX12772 Sequence AR054021 Sequence AR124952 Sequence AR17299 Sequence AR17299 Sequence BD243042 Antisense CQ76541 Sequence E58777 Screening m I52011 Sequence E58777 Screening m I52011 Sequence AR3300885 Sequence AR33772 Sequence AX839772 Sequence AX839772 Sequence AX839772 Sequence AX839772 Sequence AX839772 Sequence AX839773 Sequence AX839772 Sequence AX839772 Sequence AX839773 Sequence AX085490 Sequence AX085490 Sequence BC013307 Homo sapi E23357 Virus vecto	DNA linear PAT 17-JUL-2003 -xL.	JP 2002519048-A 4 02-JUL-2002; STEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK tifficial Sequence 2002519048-A/4 -2012-1903 JP 2000557839 -JUL-1998 US 09/109614 A STEIN 09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC /42, 11K47/48,A61K48/00,A61P35/00,C12N15/00 TISENSE OLIGONUCLEOTIDE Location/Qualifiers 1. 20	lo; hes 0; Indels 0; Gaps 0;
100.0 702 9 BT007208 100.0 723 9 HSU72398 100.0 724 6 AX127722 100.0 926 6 AR18504 100.0 926 6 AR18504 100.0 926 6 AR124952 100.0 926 6 AR124311 100.0 926 6 AR172594 100.0 926 6 AR172594 100.0 926 6 AR172594 100.0 926 6 AR391062 100.0 926 6 AR391063 100.0 1256 6 AX095490 100.0 2575 6 CQ827863 100.0 7372 6 E23357	ALIGNMENTS BD235152 20 bp DNJ Oligonucleotide inhibitors of bcl-xL. BD235152 JP 2002519048-A/4. Synthetic construct synthetic construct artificial sequences. 1 (bases 1 to 20) Stein, C.A. Oligonucleotide inhibitors of bcl-xL	3 TRUD JPRU 022 022 022 022 033 046 AN AN AN AN AN AN AN AN AN AN AN AN AN	Marty 100.0%; Fred. No. Conservative 0; Mismatch GCGATCCGACTCACCAAT 20
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Compugen Ltd. Compugen Ltd. Search time 480.738 Seconds (without alignments) 1967.381 Million cell updates/sec seidues neters: 9053458		chance to have result being p letribution. Description. Description. BD235152 BD235167 CQ136574 CQ13659477 CQ273477 CQ273477 CQ2736704 CQ136611 CQ136611 CQ136611	CQ298444 Sequence CQ335104 Sequence BD097037 A BH4 fus BD084108 Method of BD102202 Method fo
GenCore version pyright (c) 1993 - 2005 search, using sw model uary 4, 2005, 18:10:39 9-753-169A-4 gcgatccgactcaccaat 20 TITY_NUC p 10.0, Gapext 1.0 729 seqs, 23644849745 re satisfying chosen parar h: 0 h: 2000000000 imum Match 10% imum Match 10% imum Match 10% imum Match 10%		he number of results predictions of the total by analysis of the total summaries of the tot	600 600 636 702 702 6
Co OM nucleic - nucleic Run on: Febr Title: US-0 Sequence: 20 Sequence: 1 ct Scoring table: IDEN Gapo Searched: 4526 Total number of hits Minimum DB seq lengt Minimum DB seq lengt Maximum DB seq lengt Maximum DB seq lengt	Database : 2 2 2 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Result Querical No. is the score greater and is derived with the score greater and is derived loss of the score of the sco	20000

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A61K47/42,
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Oligonucleotide inhibitors of bcl-xL
Patent: JP 2002519048-A 19 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
NN JP 2002519048-A/19
PD 02-JUL-1908
PP 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
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                                                              BD235167 20 bp DN Oligonucleotide inhibitors of bcl-xL.
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/db_xref="taxon:32630"
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modified_base (13)..(1:
modified_base (15)..(1:
Location/Qualifiers
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  1 CTGCGATCCGACTCACCAAT 20
                                                                                                BD235167.1 GI:33044937
JP 2002519048-A/19.
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synthetic construct
artificial sequences.
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Matches 20; Conserv
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SOURCE
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                                   RESULT 2
BD235167
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CQ113695
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HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
patent: WO 0157276-A 22596 09-AUG-2001;
                                                                                                                         probes useful
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                                                                                      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid analysis of gene expression in human placenta Patent: WO 0157272-A 22554 09-AUG-2001; Aeomica, Inc. (US)
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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Location/Qualifiers
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LOCUS DEFINITION

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KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE

JOURNAL

REFERENCE

source

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PAT 23-JAN-2004
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/db_xref="taxon:9606"
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HIT: BE227063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
Patent: WO 0186003-A 21963 15-NOV-2001;
Aeomica, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human fetal liver
Patent: WO 015/277-A 21738 09-AUG-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Location/Qualifiers
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CQ273477
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      PAT 21-JAN-2004
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HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER-130-PB 0004 WO 3<br/>
3<150-US 60/180, 312<br/>
3<150-US 60/180, 312<br/>
456-L151-S 6 May 2000 (26.05.00)<br/>
456-L152-S 6 May 2000 (26.05.00)<br/>
456-L152-S 6 May 2000 (26.05.00)<br/>
450-L150-US 60/236, 359<br/>
450-L150-US 60/236, 359<br/>
403-L10.00)<br/>
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
analysis of gene expression in human heart
Patent: WO 0157274-A 17227 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 17227 from Patent WO0157274.
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/organism="Homo sapiens"
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/note="MAP TO AL117381.9~EXPRESSED IN BONE MARROW, SIGNAL
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BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0.99"
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Human genome-destived single exon nucleic acid probes useful for
analysis of gene expression in human brain
Patent: WO 0157275-A 21867 09-AUG-2001,
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CQ347773 GI:41296844
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/organism="Homo sapiens"
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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

ANALYZISIS OF GENE EXPRESSION IN HUMAN ADULT LIVERAL3D> PB 0004 WO

34.150 US 60/180, 312.4151> 04 February 2000 (04.02.00)<150> US

60/207, 456.151> 26 May 2000 (26.05.00)<150> US 09/632,366.151> 03

AUGUST 2000 (03.08.00)<150> GB 24.263.6.151> 03 October 2000

(33.10.00)<150> US 60/236,359.511> 27 September 2000

(21.09.00)<150> US 60/236,859.511> 27 September 2000

(21.09.00)<150> US 60/236,869.408.151> 30 June 2000 (30.06.00)<170>

Molecular Dynamics Sequence Listing Engine

Aeomica, Inc. (US)

Location/Qualifiers
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/organism="Homo sapiens"
/organism="Homo sapiens"
/or Lype="unassigned DNA"
/db xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN ADULT LIVER, SIGNAL = 1.7"
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/db xref="taxon)9606"
/nove="MAP TO AL117381.9~EXPRESSED IN FETAL LIVER, SIGNAL
= 3.5"
                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver
Patent: WO 0157277-A 9222 09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                   Sequence 9838 from Patent W00157273.
CQ222999
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Sequence 9222 from Patent WO0157277.
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/organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                CQ222999.1 GI:41205280
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CQ260961.1 GI:41233441
                                                                                                                                                         Homo sapiens (human)
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            RESULT 13
CQ222999
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PAT 23-JAN-2004
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type='unassigned DNA"
/db_xref='traxon:9606'
/note="MAP TO AL117381.9~EXPRESSED IN LUNG, SIGNAL = 2"
                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung Patent: WO 186603-A 9549 15-NOV-2001; Aeomica, Inc. (US) Location/Qualifiers
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                                                                                                                               linear
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                                                                                                                          CQ298444 600 bp DN
Seguence 9549 from Patent WO0186003.
CQ298444
CTGCGATCCGACTCACCAAT 101
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model	n on: February 4, 2005, 15:50:53 ; Search time 258.033 Seconds (without alignments) 406.880 Million cell updates/sec	Title: US-09-753-169A-4 Perfect score: 20 Sequence: 1 ctgcgatccgactcaccaat 20	Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	Searched: 4134886 segs, 2624710521 residues	Total number of hits satisfying chosen parameters: 8269772	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : N_Geneseq_23Sep04:* 1.
	OM nu	Run on:	Title: Perfec Sequen	Scorin	Searc	Total	Minim Maxim	Post-1	Databi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz46974 Bcl-Xl mR	Adk66040 Standardi	Adk66037 Standardi	Ach46093 Human inf	Aba73433 Human foe	Aai53868 Probe #22	Aba38761 Probe #17	Aak48039 Human bon	Aak21876 Human bra	Abs47753 Human liv	Abs21972 Human gen	Ach87595 Human gen	Aba60917 Human foe	Aai40812 Probe #94	Aba28894 Probe #73	Aak35096 Human bon	Aak09207 Human bra	Abs34848 Human liv	Abs09558 Human gen	Aah48169 Mutant bc	Aah43464 cDNA clon
SUMMARIES	ΩI	AAZ46974	ADK66040	ADK66037	ACH46093	ABA73433	AA153868	ABA38761	AAK48039	AAK21876	ABS47753	ABS21972	ACH87595	ABA60917	AAI40812	ABA28894	AAK35096	AAK09207	ABS34848	ABS09558	AAH48169	AAH43464
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Add65218 Human Bcl Adg65218 Human Bcl Adg65209 Human Bcl Adg65209 Human bcl Adg6209 Human thy Adt40079 Bcl-XL ge Adz93614 Bcl-XL ge Adz9314 Bcl-XL ge Adz15189 Human bcl Adx6679 Human bcl Adx66187 Human bcl Adx6679 Human cDN Adx1104 Human cDN Adx13104 Human RCD Adx1351 Renal cel Adx01990 Human RCD Adx1351 Renal cel Adx01990 Human PRO Adx31182 Base sequ Abk52490 Fluxese ce Adx52490 Fluxese b Adx52430 Chinese b	NTS).	LUMBIA NEW YORK. 1 ligonucleotides inhibiting the anti-apoptotic protein bcl-reducing bcl-xL production in tumor cells to treat cancer cells to promote the regression of vascular lesions. 69pp; English. rovides antisense oligonucleotides or their derivatives eliminate expression of the anti-apoptotic protein bcl-clotides can be introduced into tumour cells to reduce on to treat cancer, especially epithelial cancer, especially epithelial cancer, e.g. or bladder cancer, oligonucleotides comprising one or more 5 propymy pyrimidiam modification may especially be used 5 of bcl-2 family proteins (to which bcl-xL belongs) in The oligonucleotides can be introduced into vascular bcl-xL production to promote the regression of vascular
ADM45994 ADG65218 ADG65209 AAC81698 AAC301079 AAC301079 AAC3011079 ABC6411 AAC30104 ADD6779 ADD72779 ADD7277	ALIGNMENTS 10 BP. 1. sense oligo D. 1. col-xL; tumour; collular lesion; an 1.250.	YORK. ides inhibiting the illar, production in comote the regression is sense oligonucleot expression of the a expression of the a cancer. Oligonucleo pyrimidine modifica pyrimidine modifica family proteins (to uncleotides can be indection to promote
114 1 2 2 2 3 2 3 2 3 3 2 3 3 3 3 3 3 3 3 3	20 BP. ry) tisense bcl-xL ascular 15250.	NEW YORK. leotides ig bcl.xL co promote English. s antisens hate expre tes can be reat canc der canc
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	ndard; I (first specific ic prote ic bcl-: r; bcl-: r; bcl r; bcl	COLUM 7140/1 714
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20 CTGCGATCCGACTCACCAAT

ss; standardized polynucleotide system; medical diagnosis; functional genomics; sample analysis.

(ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.

Koehler T, Rost A;

28-FEB-2002; 2002DE-01009071.

DE10209071-A1 Unidentified

25-SEP-2003

28-FEB-2002; 2002DE-01009071.

Standardized polynucleotide system polynucleotide #8.

(first entry)

06-MAY-2004

ADK66037;

BP

ADK66037 standard; DNA; 337

RESULT 3 ADK66037/c

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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpytydyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-Xi mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              medicine, functional genomics, clinical pharmacology, pharmacogenetics, pharmaceutical testing, analysis of food or environmental samples and also for ultra-sensitive detection of proteins by immuno-PCR. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unctional genomics; sample analysis; pharmacogenomics; sample analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is a probe used to isolate a polynucleotide used in the system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Standardized polynucleotide system, useful for quantitative, real-time determination of nucleic acid, comprises stabilized standards, primers
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                                                                                                                                   Query Match 100.0%; Score 20; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                        ADK66040 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Standardized polynucleotide system, useful for quantitative, real-time determination of nucleic acid, comprises stabilized standards, primers
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Matches 20; Conservative
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Gaps

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100.0%; Score 20; DB 10; Length 25; 100.0%; Pred. No. 1.2; ive 0; Mismatches 0; Indels

Local Similarity 100. nes 20; Conservative

Matches

Query Match

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n genome-derived single exon nucleic acid probes useful for analyzing expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #22554 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
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2000US-0234687P.
                                                                                                                                                                                                                                                                               27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                 30-JAN-2001; 2001WO-US000669
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                                                                                                                                                                                             2000US-0207456P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52
                                              WO200157277-A2
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      Homo sapiens.
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03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                     03-AUG-2000;
                                                                                                                                                                                                                                                             21-SEP-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2001
                                                                                                                                                                                             26-MAY-2000;
                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI53868;
                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynuclectide comprising any one of 38043 CDNA sequences, appearing as AFH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence ewas carding frame of the novel polynucleotide. The nucleic acid sequences a reading frame of the novel polynucleotide. The nucleic acid sequences in description of the novel polynucleotide. The nucleic acid sequences in formal polynucleotide. The nucleic for general desorters and other traits. The nucleotide in forensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations capponible for generic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of sequences in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense bNA or RNA. The present sequence is useful for generating antisones specific for it. The present sequence is one of the 38043 isolated obNA/EST sequences. Note: The sequence data charactering antisoners are sequenced that the patent did not form part of the printed specification, but was obtained in electronic format discounting the propertices.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                            Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human foetal liver single exon nucleic acid probe #21738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stache-Crain B, Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 33305; 44pp; English.
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Human infant brain cDNA #156.
                                                                                                                                                                                                                                   0-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995
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                                                                                                                                                                                                                                                                                                                                                               STACHE-CRAIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labat I,
                                                                                                                                                                                                                                                                                                                                                                                      DICKSON M C. JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antisense DNA or RNA
                                                                                                                                                                                                                                                                                                                         DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-615964/58.
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les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                LABAT I.
                                                                                                                                                  US2003073623-A1
                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                           17-APR-2003.
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                                                                                                                                                                                                                                                                                                                                           (LABA/)
(STAC/)
(DICK/)
(JONE/)
                                                                                                                                                                                                                                                                                                                       DRMA/)
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Gaps

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Indels

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0; Mismatches

BP.

RESULT

0×2×6×8×8×

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Score 20; DB 4; Length 555; Pred. No. 1.6;

Wed Jul 13 12:32:02 2005

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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #17227 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 4; Length 555; 100.0%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 22554; 654pp; English.
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                                                                                                                                                        Rank DR;
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                                                                                                                                                                                                                                                                                                          gene expression in human placenta.
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                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                        Chen W,
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                             WPI; 2001-488897/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
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           present sequence is one such probe. The probes may be used for present sequence is one such probe. The probes may be used for from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for analyzing
measuring human gene expression in a sample derived from human heart. The
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful gene expression in human bone marrow.
                                                                                                                                                                                                                              100.0%; Score 20; DB 4; Length 555; 100.0%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 555;
                                                                                                                                                                                             Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                 0; Indels
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Pred. No. 1.6;
                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                    1 CTGCGATCCGACTCACCAAT 20
                                                                                                                                                                                                                                                                                                                                     82
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26-MX-2000; 2000US-0204465P.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00234559P.
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                                                                                                                                                                                                                                                                                                                        63 CTGCGATCCGACTCACCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                 20; Conservative
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                                                                                                                                                                                                                                                  Local Similarity
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Best Local Similarity
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Gaps

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us-09-753-169a-4.rng

Matches

RESULT 9 AAK21876

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measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is sesociated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a single exon nucleic acid probe (SENP) (1) for
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                                                                            Human; single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 4; Length 555; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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                                      Human liver single exon probe, SEQ ID No 22743.
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2000US-00608408.
2000US-00632366.
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
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21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
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Matches

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Gaps

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tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Budlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; nyaline membrane disease; open reading frame; ORF measure gene expression in human lung samples Chen W, Rank DR; (MOLE-) MOLECULAR DYNAMICS INC 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263. 30-JAN-2001; 2001WO-US000665 04-FEB-2000; 2000US-0180312P 26-MAY-2000; 2000US-0207456P 30-JUN-2000; 2000US-00608408 03-AUG-2000; 2000US-00632366 Hanzel DK, WPI; 2002-114183/15 WO200186003-A2 Homo sapiens. 15-NOV-2001, Penn SG,

Spatially-addressable set of single exon nucleic acid probes, used to

Claim 4; SEQ ID NO 21963; 634pp; English.

Penn SG, Rank DR, Hanzel DK,

WPI; 2004-119264/12.

03-APR-2002; 2002US-00029386. 03-APR-2002; 2002US-00029386.

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 complements or the 12387 open reading frames derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a a collection of detectably labeled nucleic acids derived from human lung makk, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably clabeled nucleic acids from eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one compassion of the exons in the specification, or encoded by the compassion of the exons in the specification.

Cof 12011 sequences, mentioned in the specification, or encoded by the cancer, chronic observative pulmonary disease such as asthma, lung derived many and for the study of lung disease such as asthma, lung dasease (LID), familial ideopathic pulmonar Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

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                                                                                Gaps
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                                               Length 555;
             Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                0; Indels
                                             100.0%; Score 20; DB 6; 100.0%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                      Human genome derived single exon probe #20790.
                                                                                0; Mismatches
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                                                                                                                                   63 CTGCGATCCGACTCACCAAT 82
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                                                                              20; Conservative
                                                           Local Similarity
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a wector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 probe cited above, and or any of the above mentioned amino acid substitutions), an equences (optionally with conservative amino acid substitutions), an expression of any of the above mentioned amino acid substitutions), and addressed application or addressed apprint at least a single exon sequences (optionally with conservative amino acid substitutions), and addressed application and addressed application and addressed applications and addressed application and addressed and addressed application and addressed application and addressed and addressed application and addressed application and addressed application and addressed application and addressed and addressed and addressed and addressed methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene New human genome-derived single exon nucleic acid probes useful for huma gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for Claim 1; SEQ ID NO 20790; 80pp; English. surveying tissues.

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Probe;
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AAI40812
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ID ABA2
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expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising streaming in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form pat of the printed specification, but was obtained in electronic format directly from USPTO at sequence.
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Pred. No. 1.6;
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                                                           Gaps
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                                                           0; Indels
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                 Score 20; DB 4
Pred. No. 1.6;
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2000US-0207456P.
2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and e.g. cardiovascular disease. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                               Probe #7360 for gene expression analysis in human heart cell sample.
                                                                   Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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21-SED-2000; 2000US-0234687P.
27-SED-2000; 2000US-0236359P.
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Gaps °, 100.0%; Score 20; DB 4; Length 600; 100.0%; Pred. No. 1.6; O; Mismatches 0; Indels Query Match
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Search completed: February 4, 2005, 21:52:41 Job time: 259.033 secs

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BQ924197 BQ927754 BM018845

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167 bp mRNA linear EST 06-MAR-2002
K-EST0088575 S20T665307 Homo sapiens cDNA clone S20T665307-9-G04
5', mRNA sequence.
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1 (bases 1 to 167)
1 (bases 2 to 167)
1 (bases 3 to 167)
2 (bases 3 to 167)
2 (bases 4 to 167)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="$20T665307-9-G04"
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Genome Research Center
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_trem=mana.
/mol_trem=mana.
/mol_trem=mana.
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="Str0298"
/note="Organ: stomach: Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                       AW820481
QV2-ST0298-140200-042-f12 ST0298 Homo sapiens CDNA, mRNA sequence.
AW820481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/soripts/gethtml2.pl?tl=&t2=QV2-ST0298-140 Seq primer: puc 18 forward
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converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                             Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                   ch 100.0%; Score 20; DB 4; Length 167; 1. Similarity 100.0%; Pred. No. 7.3; 20; Conservative 0; Mismatches 0: Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                                  136 CTGCGATCCGACTCACTAT 117
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Homo sapiens
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Best Local 9
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AUTHORS
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PUBMED
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Gaps

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0; Indels

Query Match 100.0%; Score 20; DB 2; Length 332; Best Local Similarity 100.0%; Pred. No. 7.7; Matches 20; Conservative 0; Mismatches 0; Indels

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/clone lib="$207665307"
//note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: Not!; The poly (A)+ RMA was dephosphoryLated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The cDNA vector was
adjusted to have about 6nnc. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-lerg method; The
                                                                                                                                                                       BM818649 396 bp mRNA linear EST 06-MAR-2002
K-EST0085991 S20T665307 Homo sapiens CDNA clone S20T665307-4-F03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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CM3-GN0297-110101-607-f03 GN0297 Homo sapiens cDNA, mRNA sequence.
BI051278
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                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Fax: +82-42-860-4409
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/db_xref="taxon:9606"
/clone="S20T665307-4-F03"
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 03
High quality sequence stop: 396.
Location/Qualifiers
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EST.
103 CTGCGATCCGACTCACCAAT
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Contact: Kim YS
                                                                                                                                                                                                                                 5', mRNA sequence.
BM818649
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BI051278
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Homo sapiens
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                                                                                 Mumalia; Butheria; Craniata; Vertebrata; Euteleostomi; Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

J. (bases 1 to 418)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 bp mRNA linear EST 18-APR-1996 za73406.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:298187 5' sīmilar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. ;, mRNA sequence. W01420 W01420.1 GI:1273428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
mail: abimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
thtp://www.ludwig.org.br/scripts/gethtm12.pl?ti=CM3&t2=CM3-GN0297-
110101-607-f03&t3=2001-01-11&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 437)

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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/clone lib="GN0297"
/note="Grgan: placenta_normal; Vector: pucl8; Site_1:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORRSTES PCR (U.S. Letters Patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 418.
Location/Qualifiers
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/db_xref="taxon:9606"
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    GI:14458808
                                                Homo sapiens (human)
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W01420/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.X., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL, contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 383.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
    Marra,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Korea Research Institute of Bioscience & Biotechnology
5.2 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 20; DB 7; Length 437;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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                                                                                        The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM818387.1 GI:19174800
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                                                                                                                                                                                                                                                                                                                                                                                                .437
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Class: exon-trapped.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                                                             Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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Matches 20; Conserv
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                                                                source
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                               /lab host="Toplop""
//lab host="Toplop""
/clone lib="$20T665307"
/clone lib="$20T665307"
/clone lib="$20T665307"
/clone lib="$20T665307"
/site_2: Not!; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR is site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of converted calls E. coli Toplof' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ537061 456 bp DNA linear GSS 06-NOV-2000 AST-2P01514.AB Genetrap PC-3 Human Prostatic Carcinoma Library Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmp-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 456)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 20; DB 4; Length 447; l Similarity 100.0%; Pred. No. 7.9; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens genomic 5', genomic survey sequence.
                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                             1. .447
/organism="Homo sapiens"
Email: yongsung@mail.kribb.re.kr
Plate: 3 row: B column: 02
High quality sequence stop: 447.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 CTGCGATCCGACTCACAAT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGCGATCCGACTCACCAAT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Greg Henkel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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AZ537061
LOCUS
DEFINITION
                                                                                                                Source
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VERSION
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SOURCE
                                                                                 FEATURES
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/tissue type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="NH10B (phage-resistant)"
/lab_host="NH MGC42"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5: adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procuremn: ArC.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1879 row: p column: 19
High quality sequence stop: 267.
High quality sequence stop: 267.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
                                                                                                                                                                                                                                                                  /note="Organ: Prostate; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and usto transform DH5-alpha competent bacteria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMO50133 478 bp mRNA linear EST 07-NOV-20
603632480F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5422338 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                  /clone_lib="Genetrap PC-3 Human Prostatic Carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 8; Length 456; 100.0%; Pred. No. 7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                        /tissue type="Adenocarcinoma"
/cell type="Epithelial"
/cell_line="PC-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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Euteleostomi;

Best Local Matches 2

8 셤 DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AW814883

ORGANISM

AUTHORS REFERENCE

JOURNAL MEDLINE PUBMED

COMMENT

TITLE

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/mol type="mrRNA"
/db xref="taxon:9606"
/dl xref="taxon:9606"
/clone="INABC:1632058"
/tlssue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH1 MGC 44"
/note="Organ: uterus; vector: poTB7; Site_1: XhoI; Site_2: BcoRI; cDNR made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
555 bp mRNA linear EST 21-JUL-2000 601310279F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632058 5', BE393580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE617040 563 bp mRNA linear EST 20-OCT-2000 601441454F1 NIH MGC_65 Homo sapiens cDNA clone IMAGE:3845892 5',
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 555)

1 (Mases 1 to 555)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Email: Gapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM322 row: m column: 19
High maslity conneases
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Rammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 563)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 555;
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0
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 551.
Location/Qualifiers
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                                                                                                                                          BE393580.1 GI:9338945
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Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR1-ST0206-120 Seq primer: puc 18 forward.
High quality sequence start: 55
High quality sequence start: 55
High quality sequence stop: 485.
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/db xref="taxon.9606"
/db xref="taxon.9606"
/db xref="taxon.9606"
/dclone lib="Sr206"
/clone lib="Sr206"
/note="Organ: stomach; Vector: puc18; Site 1: Smal;
Site 2: Smal; A min1-library was made by cloning products
Site 2: Smal; A min1-library was made by cloning products
derived from ORENTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                                                                                                                                  AW814883 486 bp mRNA linear EST 17-MAY-2000
MR1-ST0206-120400-022-£04 ST0206 Homo sapiens CDNA, mRNA sequence.
AW814883
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 486)
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baboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                 Pred. No.
                                                                                                                               242 CTGCGATCCGACTCACCAAT 223
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                            ilarity 100.0%; P:
Conservative 0;
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/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:3845892"
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/clone_lib="NIH MGC_65"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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K-EST0013545 S6SNU620 Homo sapiens cDNA clone S6SNU620-6-A10 5',
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
http://image.llnl.gov k column: 13
Plate: LLAMSST row: k column: 13
High quality sequence stop: 561.
Location/Qualifiers
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Fax: +82-42-860-4409
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/cell type="Scattering floating"
/cell line="SNU-620"
/lab_nost="ToplOF"
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Unpublished (2002)
Contact: Kim YS
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/organism="Homo sapiens"
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Plate: 6 row: A column: 10
High quality sequence stop: 579.
Location/Qualifiers
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/clone="S6SNU620-6-A10"
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/Jab host="Top10F" |
/clone lib="S20T665307" |
/clone lib="S20T665307" |
/clone lib="S20T665307" |
/clone lib="S20T665307" |
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The pol; (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR is the by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector was corrected to a DNA strand by Okayama Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method.
intact mRNA was ligated with DNA-RNA linker including BCOR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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K-EST00088533 S20T665307 Homo sapiens CDNA clone $20T665307-9-C10
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yusecng-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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100.0%; Pred. No. 8.1
:ive 0; Mismatches
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/clone="$20T665307-9-C10"
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/organism="Homo sapiens"
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Plate: 9 row: C column: 10
High quality sequence stop: 620.
Location/Qualifiers
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Contact: Kim YS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CONA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library
Arrayed by: The I.M.A.G.E. Consortium (LiMI)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
image.llnl.gov/image/html/iresources.shtml
Seq primer: 40RP from Gibco
High quality sequence stopp: 450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 06-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="MGLO"
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/lab host="MIJUBE (phage-resistant)"
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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
FooR; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 657)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Other_ESTs: ba09f05.x1
                                                                                                                     Gaps
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The cDNA libraries constructed by this method are full-length enriched cDNA library."
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                                                                           DB 4; Length 620;
8.1;
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'cell_line="MGC3"
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100.0%; Pred. No. 8.1
:ive 0; Mismatches
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BE207063/c
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// Organism="nome saplems"
// Ab_xref="taxon:9606"
// Clone="INARA"
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// Lissue_type="CNCAP(3)T-225 cell line"
// Lib host="DH10B (T1 phage resistant)"
// Lib host="DH10B (T2 phage resistant)
// Lib host="DH20B (T2 ph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa 375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA Tel: 319 335 9256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue procurement: Tim Ratlift
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pXx-5.
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 681)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
UI-HF-CB0-atf-g-11-0-UI.r1 NIH_MGC_210 Homo sapiens cDNA clone
IMAGE:30570802 5', mRNA sequence.
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Pred. No. 8.2;
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BT008248 Synthetic
U72398 Human Bcl-x
AR054022 Sequence
AR172595 Sequence
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AR380913 Sequence
AX127722 Sequence
AX12772 Sequence
AR118504 Sequence
AR144915 Sequence
AR172594 Sequence
AR172594 Sequence
BD243042 Antisense
CO765842 Sequence
ES8777 Screening m
IS2011 Sequence
ES8777 Screening m
IS2011 Sequence
AR39772 Sequence
AR39772 Sequence
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Z23115 H.sapiens
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staten: JP 2002519048-A S 02-UUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
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02-JUL-1998 US 09/1096:
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                                           HSU72398
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AR371662
AR380913
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RESULT 1
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          5.1.6
Compugen Ltd.
                                                                                                                                                                                                                   4526729 seqs, 23644849745 residues
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
          GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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CQ298444
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PAT 21-JAN-2004

LOCUS DEFINITION ACCESSION VERSION

RESULT 2 BD235168

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ORGANISM

KEYWORDS SOURCE

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

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/mol_type="unassigned DNA"
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/nofe="MAP TO ALI17301.9-EXPRESSED IN PLACENTA, SIGNAL = 0.99-SWISSPROT HIT: 070117, EVALUE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72399.1, EVALUE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
Patent: WO 0157276-A 22596 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Human genome-destived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 22554 09-AUG-2001;
                                                                                                                                                                            Length 512;
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100.0%; Pred. No. 2e+02;
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100.0%; Pred. No. 2e+02;
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Sequence 22596 from Patent WO0157276.
CQ152574
CQ152574.1 GI:41159924
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    .555
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/mol_type="unassigned DNA"

                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="taxon:9606"
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/organism="Homo sapiens"
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Location/Qualifiers
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Matches 18; Conservative
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TITLE
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Patent: JP 2002519048-A 20 02-JUL-2002;
HF TRUGIESE OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/20
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PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 13703 from Patent WO02068579.
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Oligonucleotide inhibitors of bcl-xL.
BD235168
BD235168.1 GI:33044938
JP 2002519048-A/20.
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misc_binding (13)...(12)
misc_binding (13)...(18).
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02-JUL-1999 JP 2000557839
02-JUL-1998 US 09/109614
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SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

FEATURES

REFERENCE

RESULT 3 CQ727769/c

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Gaps ; 0 PAT 21-JAN-2004

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PAT 23-JAN-2004

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1.:555
/organism="Homo sapiens"
/ml type="unassigned DNA"
/db xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN FETAL LIVER, SIGNAL
= 3.5-SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST_HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine Patent: WO 0157273-A 22743 09-AUG-2001;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                   ; Score 18; DB 6;
; Pred. No. 2e+02;
0; Mismatches 0
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CQ273477
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Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 18; Conservative 0;
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Matches 18; Conservative
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/mol_type="unassigned DNA"
/db_xref="taxon:966"
/db_xref="taxon:966"
/note="MAP_TO AL117381"
1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE
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             /noce="MAP TO AL117381.9~EXPRESSED IN BONE MARROW, SIGNAL
= 4.7~SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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HUMAN GENOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER-130- PB 0004 WO
3<150- US 60/180,312-151- 04 February 2000 (04.02.00)<150- US
60/207,456-151- 26 May 2000 (26.05.00)<150- US 09/632,366-151- 03
August 2000 (03.08.00)<150- GB 24263.66151- 03 October 2000
(03.10.00)<150- US 60/236,359-151- 27 September 2000
(27.09.00)<150- US 60/234,687-151- 21 September 2000
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0157274-A 17227 09-AUG-2001;
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larity 100.0%; Pred. No. 2e+02;
Conservative 0; Mismatches 0
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Sequence 22743 from Patent WO0157273.
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Sequence 17227 from Patent WO0157274.
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/ Organism="Homo sapiens"

/mol_type="unassigned DNA"

/mb xref="texon:9606"

/note="MAP TO AL117381.9~EXPRESSED IN BRAIN, SIGNAL =

/note="MAP TO AL117381.9~EXPRESSED IN BRAIN, SIGNAL =

1.6~SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN HIT:

BE207063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE

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/organism="Homo sapiens"
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/db xref="texon:9606"
/nole="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
2-SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN HIT:
BE207063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung
Patent: WO 186003-A 21963 15-NOV-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human brain
Patent: WO 0157275-A 21867 09-AUG-2001;
Aeomica, Inc. (US)
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llarity 100.0%; Pred. No. 2e+02;
Conservative 0; Mismatches 0; Indels
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1 Similarity 100.0%; Pred. No. 2e+02;
18; Conservative 0; Mismatches 0; Indels
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Sequence 21867 from Patent WO0157275.
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CQ347773.1 GI:41296844
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Sequence 9498 from Patent WO0157272.
CQ100639.1 GI:41069665
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analyais of gene expression in human placenta
Patent: WO 0157272-A 9498 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Human genome-derived single exon nucleic acid probes useful for
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 9653 09-AUG-2001;
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0
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Sequence 7360 from Patent W00157274.
CQ175964
CQ175964.1 GI:41170703
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Location/Qualifiers
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Best Local Similarity 100.
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Matches 18; Conservative
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Search completed: February 4, 2005, 23:30:40 Job time: 432.664 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
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= 1.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVERA130- PB 0004 WO 3-150- US 60/180,312-151- 04 February 2000 (04.02.00)-150- US 60/207,456-151- 26 May 2000 (26.05.00)-150- US 09/632,366-151- 03 August 2000 (03.08.00)-150- GB 24563 66151- 03 Gotcher 2000 (33.10.00)-150- US 60/236,359-151- 27 September 2000 (27.09.00)-150- US 60/236,359-151- 21 September 2000 (27.09.00)-150- US 90/608,408-151- 30 June 2000 (30.06.00)-170- Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 9838 09-AUG-2001;
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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analysis of gene expression in human heart
Patent: WO 0157274-A 7360 09-AUG-2001;
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Sequence 9222 from Patent W00157277.
CQ260961
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Sequence 9838 from Patent WO0157273.
                                    Inc. (US)
Location/Qualifiers
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Location/Qualifiers
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CQ222999.1 GI:41205280
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AUTHORS
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CQ222999
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/db_xref="taxon:9606"
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= 3.5"
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver

Patent: WO 0157277-A 9222 09-AUG-2001;

Aeomica, Inc. (US)

Location/Qualifiers
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100.0%; Score 18; DB 6; Length 600;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
                                                                       OM nucleic - nucleic search, using sw model
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4, 2005, 15:50:53 February Run on:

; Search time 232.23 Seconds (without alignments) 406.880 Million cell updates/sec

US-09-753-169A-5 18 Title:

1 agtectgttetetteeac 18 Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4134886 seqs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04:* Database :

geneseqn1980s:

geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2002as: geneseqn2003as: geneseqn2003bs: geneseqn2002bs: geneseqn2001bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn20048:

SUMMARIES

Result No.	Score	Query	Query Match Length	DB	ΠD	Description
1	18	100.0	18	3	AAZ46975	Aaz46975 Bcl-Xl mR
7	18	100.0	555	4	ABA73433	Aba73433 Human foe
е	18	100.0	555	4	AAI53868	Aai53868 Probe #22
4	18	100.0	555	4	ABA38761	Aba38761 Probe #17
2	18	100.0	555	4	AAK48039	Aak48039 Human bon
9	18	100.0	555	4	AAK21876	Aak21876 Human bra
7	18	100.0	555	4	ABS47753	Abs47753 Human liv
80	18	100.0	555	φ	ABS21972	Abs21972 Human gen
σ	18	100.0	559	12	ACH73889	Ach73889 Human gen
10	18	100.0	564	12	ACH87595	Ach87595 Human gen
11	18	100.0	009	4	ABA60917	Aba60917 Human foe
12	18	100.0	009	4	AAI40812	Aai40812 Probe #94
13	18	100.0	600	4	ABA28894	Aba28894 Probe #73
14	18	100.0	600	4	AAK35096	Aak35096 Human bon
15	18	100.0	600	4	AAK09207	Aak09207 Human bra
16	18	100.0	009	4	ABS34848	Abs34848 Human liv
17	18	100.0	600	9	ABS09558	Abs09558 Human gen
c 18	18	100.0	989	4	AAH48169	Aah48169 Mutant bc.
c 19	18	100.0	702	ß	AAH43464	Aah43464 cDNA clon
c 50	18	100.0	702	12	ADM45994	Adm45994 Human apo
c 21	18	100.0	737	~	AAQ81699	Aaq81699 Human thy

Abz83507 Toxicolog	Adi32132 Human cDN	Adg65218 Human Bc]	Aaf30926 Human Bcl	Adg65209 Human Bc	Aaq81698 Human thy	Aat40079 Bcl-XL ge	Aaz93614 Bcl-x ge	. Aas15189 Human bo	Human	Abk84766 Human cDN	Abt16641 Human bc]	Add56779 Human bc	Aad64187 Human bc]	Adi32104 Human cDN	Adh52630 Human ant	Ado19990 Human PR(Adpl3351 Renal ce	Aas00247 Bcl-Xl-DT	Aas00250 LFn-Bcl-X	Adg89403 Cancer de	Adn04260 Antipsor	Ado19866 Human PR	Aax33182 Base sequ
507	132	218	26	209	98	79	14	. 68	10	99	41	179	187	104	630	990	351	47	20	403	260	998	82
ABZ83507	ADI3213	ADG65218	4AF30926	ADG65209	\ A Q81698	AT40079	AAZ93614	AS15189	AAC9081(4BK84766	ABT16641	ADD56779	AAD64187	ADI32104	ADH5263	ADO1999	ADP1335	AS0024	AS0025C	ADG89403	ADN0426	ADO19866	AX33182
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ALIGNMENTS

AAZ46975 standard; DNA; 18 BP AAZ46975; AAZ46975

(first entry) 14-APR-2000 Bcl-X1 mRNA specific antisense oligo E.

Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss.

Homo sapiens,

WO200001393-A2.

13-JAN-2000.

99WO-US015250. 02-JUL-1999; 98US-00109614. 02-JUL-1998; (UYCO) UNIV COLUMBIA NEW YORK.

Stein CA;

WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

xL. The oligonucleotides can be introduced into the light of the light invention provides antisense oligonucleotides or their derivatives ch reduce or eliminate expression of the anti-apoptotic protein bcl-The oligonucleotides can be introduced into tumour cells to reduce which

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(first entry)

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genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                          Probe #22554 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                         Probe; microarray; human; placenta; antenatal diagnosis;
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30-UIN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
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                                                                                                         AAI53868 standard; DNA; 555
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                                                                                                                                                                                                                                                                                                                                    genetic disorder;
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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpytydyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-X1 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                        Query Match
100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal liver single exon nucleic acid probe #21738.
                                                                                                                              Sequence 18 BP; 2 A; 7 C; 2 G; 7 T; 0 U; 0 Other;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-06608408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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ACC ABA7
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DR; Rank

Chen W,

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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #17227 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, gene expression, heart, microarray, vascular system, probe, cardiovascular disease, hypertension, cardiac arrhythmia, congenital heart disease, ss.
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                                                                                                                                                                                                                         100.0%; Score 18; DB 4; Length 555; 100.0%; Pred. No. 46;
                                                                                                                                                                              Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        0; Indels
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Claim 25; SEQ ID NO 22554; 654pp; English.
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hes 18; Conservative
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460 AGTCCTGTTCTCTTCCAC 477

1 AGTCCTGTTCTCTTCCAC 18

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human brains.
                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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Pred. No. 46;
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                                                                                                                                           Rank DR;
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                                                                                                                                                                                                                                  gene expression in human bone marrow
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                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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30-JUN-2000; 2000US-00608408.
03-MG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359F.
04-OCT-2000; 2000GB-00024263.
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2000US-0236359P
2000GB-00024263
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2000US-00608408
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Best Local Similarity 100.0.
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                                                                                                                                           Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to single exon nucleic acid probes for
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27-SEP-2000; 2000US-0236359P.
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2000US-0207456P.
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26-MAY-2000; 2000US-0207456P.
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1es 18; Conservative
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                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488899/53.
                                   WO200157274-A2
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sapiens
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                                                              probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe (SENP) (I) for
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                                                   present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hyperlipoproteinaemia;
                Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English
                                                                                                                                                                                                                       100.0%; Score 18; DB 4; Length 555; 100.0%; Pred. No. 46;
                                                                                                                                                                                     Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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30-UUN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0236359P.
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les 18; Conservative
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                                                                                                                                     epilepsy a
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liver single exon nucleic acid probes of the invention. Note: The agequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiccytosis; lymphangioleionyomicosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
                                                                                                                                                             Gaps
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                                                                                                                          Length 555;
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                                                                                                                        100.0%; Score 18; DB
100.0%; Pred. No. 46;
ive 0; Mismatches
                                                                                        Sequence 555 BP; 105 A; 178 C; 139 G; 133
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2000US-00608408.
2000US-00632366.
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2000US-0236359P
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                                                                                                                                                                                                                                   460 AGTCCTGTTCTTCCAC
                                                                                                                                                                                                                                                                                                                           ABS21972 standard; DNA; 555
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                           Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-114183/15.
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27-SEP-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                               ABS21972;
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                                                                                                                                                                                                                                                                                       RESULT 8
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algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNAh, to a single exon probe, chaving a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon correctarys having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one compression of the exons in the specification, or encoded by the exons should be assigned to a single gene; a peptide comprising one compression and for the study of lung disease such as atthma, lung cancer, chronic obstructive pulmonary disease such as atthma, lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, children and provided and provided and provided and provided and provided and pulmonary fibrosis, neurofibromatosis, children and provided and for the study of lung disease (COPD), interstitial lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung and provided and provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histicorycosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
         probe of the
                                             identifying exons in a eukaryotic genome, comprising
             each
measuring the label detectably bound to
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Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

DB 6; Length 555; 0; Indels 46; Mismatches 100.0%; Score 18; Query Match
Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0; 460 AGTCCTGTTCTCTTCCAC 477 1 AGTCCTGTTCTCTTCCAC 18 g ઠે

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Gaps

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ACH73889 standard; DNA; 559 BP. RESULT 9 ACH73889 ΩX

ACH73889;

(first entry) 29-JUL-2004 Human genome derived single exon probe #7084.

Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.

Homo sapiens

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative

for assessing genomic alterations or as tools for invention relates to a nucleic acid probe for Claim 15; SEQ ID NO 7084; 80pp; English. events, aplicing

gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately can and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a method of exon microarray for measuring human gene expression, a method of exon microarray for measuring human gene expression, a method of exon probes or microarrays to contiguous amino acids of any of the above mentioned amino acid above, contiguous amino acids of any of the above mentioned amino acid above, a contiguous amino acids of any of the above mentioned amino acid above, contiguous amino acids of any of the above mentioned amino acid above, contiguous amino acids specifically to a peptide cited above, contiguous acids of sequences (optionally with conservative amino acid substitutions), and isolated antibody that binds specifically to a peptide cited above, contiguous acids and acids acids a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable customs acids including data on the expression of a single exon probe cited above. The probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the probes may be used in identifying and characterising and the addition, the probes are used in identifying and characterising smaller genomic alterations, in priming the synthesis of mucleic acids, or i expression, comprising any of the 27,400 fully defined nucleotide agequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human segdata.uspto.gov/seguence.html?DocID=20030194704

Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 18; DB 12; Length 559; larity 100.0%; Pred. No. 46; Conservative 0; Mismatches Local Similarity es 18; Conserv Query Match Matches

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RESULT 10 ACH87595 ACH87595;

BP

ACH87595 standard; DNA; 564

(first entry) 29-JUL-2004 Human genome derived single exon probe #20790.

Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.

Homo sapiens.

US2003194704-A1

16-OCT-2003

03-APR-2002; 2002US-00029386

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                                                                                                                                                                                                                                                                           control in the specification, or their complements or fragments, and expension, comprising any of the 27,400 fully defined nuclectide sequences in the specification, or their complements or fragments, and conding at least 8 amino acids of any of the 6888 amino acids sequences fully defined in the specification. The probe is a single exon probe that the specification. The probe is a single exon probe that complements of molecule expressed in human cells or tissues. Also included are a spatially.

Complementally isolatable or amplifiable from the plurality of probes cited above, where each of the plurality of probes is separately exon microarray for measuring human gene expression, a wector comprising at least 8 exon microarray for measuring human gene expression, a method of measuring human gene expression, a wector comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid substitutions), an contiguous amino acids of any of the above- mentioned amino acid substitutions of solated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying expression analysis. The probes may be used as tools for surveying capterations in the genomic locus that includes their exon, in assessing conference of expression of a single exon in a method of a nuclear expressing the operator in constructing genome-desired sof microarrays. In addition, the probes are used in identifying and contains a human gene expressing the oper-encoded peptide cited above. The genemic lo
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                                                                                                                                                          human
                                                                                                                                                        human genome-derived single exon nucleic acid probes useful for huma
e expression analysis, for identifying or characterizing alternative
icing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                      invention relates to a nucleic acid probe for measuring human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human foetal liver single exon nucleic acid probe #9222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 20790; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 AGTCCTGTTCTTCCAC 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGTCCTGTTCTCTTCCAC 18
                                                                                           DK;
03-APR-2002; 2002US-00029386
                                                                                             Hanzel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
                           (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                         WPI; 2004-119264/12
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                                                                                           Penn SG, Rank DR,
                                                                                                                                                                                                          surveying tissues.
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                                                                                                                                                                                       splicing
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expression in human fetal liver.
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #9498 used to measure gene expression in human placenta sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK, Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456P.
                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000669.
                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                      2000US-0207456P.
2000US-00608408
                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000; 2000US-00632366
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483447/52.
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                                                                                                          WO200157277-A2
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                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
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Gaps

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly, from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed single exon probe SEQ ID NO: 9653
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                                                                                                                                                                                                                                            100.0%; Score 18; DB 4; Length 600; 100.0%; Pred. No. 47;
                                                                                                                                                                                                               Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                          Mismatches
   Claim 1; SEQ ID NO 7360; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression in human bone marrow
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                                                                                                                                                                                                                                                                                                        1 AGTCCTGTTCTTCCAC 18
                                                                                                                                                                                                                                                                                                                                                                                                              AAK35096 standard; DNA; 600 BP.
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2000US-0234687P.
2000US-0236359P.
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2000US-0207456P.
2000US-00608408.
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                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 18; Conservative
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 47;
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                                                                                                                                                                                                                          Claim 25; SEQ ID NO 9498; 654pp; English.
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            03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234667P.
25EP-2000; 2000US-0236359P.
04-OCT-2000; 2000CB-00024263.
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2000US-00608408.
2000US-00632366.
30-JUN-2000; 2000US-00608408
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2000US-0236359P.
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Best Local Similarity 100.
Matches 18, Conservative
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                                                                Gaps
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Query Match
100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels
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26-MAY-2000; 2000US-0270456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359F.
04-OCT-2000; 2000US-0236359F.
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GenCore version 5.1.6
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Listing first 45 summaries
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657 2 BE207063 671 2 AW814739 688 4 BG708652 702 6 CF125275 707 6 CD636467 720 2 BE782474 720 2 BF782921 737 2 BF782921 737 4 B1562819 735 6 CD641746 735 6 CD641746 735 7 CK000319 821 7 CK000319 831 7 CC619432 831 7 CC619432 834 4 B1550492	AM147015 AW247015 AW26 AW247015 AW26 AW247015 AW26 AW247015 AW26 AW247015 AW26 AW247015 AW26 AW26 AW247015 AW26 AW26 AW26 AW247016 AW26 AW
18 1000.0 18 100	AW247015 BRNA SEQUENCE. AW247015.1 GI:659000 EST. Homo sapiens (human) Homo sapiens ENATYOLE (HESTOR) I (bases 1 to 279) NIH-MGC http://mgc.nc) NIH-MGC http://mgc.nc) NIH-MGC http://mgc.nc) NIH-MGC http://mgc.nc) NIH-MGC http://mgc.nc) Contact: Robert Strail Tissue Procurement: Hrish Procurement: Incompliant (LNL) DN Project Clone distrib De found through the www-bio.llnl.gov/bbrg Scores: PHRED from Up Frimming: crose HrED from Up PHRAP suite. Polly-T- Drosophila Genome Par High quality sequence Location/Quality sequence Location/Consering And Location/Consering Location/Conse
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
L bases I to 395)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., G. Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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IL5-WT0262-290301-406-g10 WT0262 Homo sapiens CDNA, mRNA sequence.
BI030877
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL5&t2=LL5-MT0262-290301-406-g10&t3=2001-03-29&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 346.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM844286 421 bp mRNA linear EST 06-MAR-2002
K-EST0122378 S12SNU216 Homo sapiens CDNA clone S12SNU216-63-B03 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                            BI030877.1 GI:14437507
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
           18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
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           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="8215NU520"
/rote="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoR1;
Site_2: NoTi; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA linker including EcoR
CDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 382)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM855440 382 bp mRNA linear EST 06-MAR-2002 K-EST0138319 S21SNU520 Homo sapiens cDNA clone S21SNU520-67-G02 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtained cDNA vectors were used for transformation of competent cells E. coli ToploF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eocun-dong Vuseong-gu, Daejeon 305-333, South Korea
Far: +82-42-860-4409
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                                                                                                                                          Length 279;
                                                                                                                                                                                                    0; Indels
                                                                                                                                             Score 18; DB 2; I
Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell type="Floating aggregates"
|cell_line="SNU-520"
|lab host="Top10F""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                                                                                                                                                                 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-67-G02"
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High quality sequence stop: 382.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: yongsung@mail.kribb.re.kr
Plate: 67 row: G column: 02
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                                                                                                                                                                                                                                                                                     161 AGTCCTGTTCTCTTCCAC 144
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100.0%;
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                                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
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source

FEATURES

Homo

SOURCE ORGANISM

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

TITLE JOURNAL COMMENT

RESULT 2 BM855440/c DEFINITION

셤 8

Matches

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Gaps

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102 AGTCCTGTTCTTCCAC 85
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//clone_libe_sizenuzie"
//clone_libe_sizenuzie"
//clone_sizenuzie Stomach; Vector: pCNS; Site_l: EcoRI;
Site_l: Not!; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
CDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60mt. The CDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
converted colls E. coli TODICF, by electroporation method.
The CDNA libraries constructed by this method are
full-length enriched CDNA library."
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 42.1)
Kim, M.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF145335 421 bp mRNA linear BST 06-AUG-
UI-HP-CB0-asn-f-06-0-UI.rl NIH_MGC_210 Homo sapiens cDNA clone
IMAGE:30569057 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                         Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 421;
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100.0%; Pred. No. 5.6e+02
ive 0; Mismatches 0
                                                                                                                                                                                                                                             21C Frontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="Lymph node"
                                                                                                                                                                                                                                                                                                                                                                                                             Email: yongsung@mail.kribb.re.kr
Plate: 63 row: B column: 03
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell type="Epithelial"
cell_line="SNU-216"
lab_host="Top10F'"
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'db_xref="taxon:9606"
               BM844286
BM844286.1 GI:19200695
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CF145335.1 GI:33260779
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Homo sapiens
                                                                             sapiens (human)
                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Kim YS
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sednence.
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                                                                             Homo
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/tissue_trype="CNCAPO" | T-225 cell line" | /tissue_trype="CNCAPO" | T-225 cell line" | /lab host="DHUOB (TI phage resistant)" | /lab host="Inhu OB (TI phage resistant)" | /lab host="Inhu OB (TI phage resistant)" | /lab host="Organ: Prostate; Vector: pT713 Pac; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand CDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand CDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT773 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratlift."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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CM3-MT0294-170101-631-c01 MT0294 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 421)
Bonaldo, M.F., Lemnon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                             Contact: Soares, MB Coordinated Laboratory for Computational Genomics
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                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30569057"
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us-09-753-169a-5.rst

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                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
Email: saimpson@ludwig.org.br
Email: saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0294-
170101-631-col&t3-2001-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 433.
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                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dc_v tagge="Adult"
/clone lib="MT0294"
/note="Organ: marrow; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 16-MAY-2004
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 474)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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17000424524125 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN422261
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    Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 7760
Fax: 650 473 7760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stringency conditions.
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/db_xref="taxon:9606"
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Best Local Similarity
''^a 18; Conserve
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20202663
10737800
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/organism="Homo sapiens"
/organism="Homo sapiens"
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/mol_type="mRNA"
/db / Lissue_type="adenocarcinoma cell line"
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/lab host="mH10B (phage-resistant)"
/lab host="mH10B (phage-resistant)"
/clone lib="NH MGC 15"
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/note="Organ: colon; Vector: poTB7; Site_1: Xho1; Site_2:
/cloned into EcoR1/Xho1 sites using the following 5;
/cloned into EcoR1/Xho1 sites using the following 6;
/cloned into EcoR1/Xho1 sites using the following 7 average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M: Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" (Aclone lib="GRN BB" /note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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I (bases I to 490)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rômail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG746308 490 bp mRNA linear EST 15-MAY-:
602703549F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856725 5'
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
eller: LLCM1708 row: a column: 14
High quality sequence stop: 464.
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thes 0;
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100.0%; Pred. No. 5.7e+02;
iive 0; Mismatches 0;
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100.0%; Pred. No. 5.7e+02
iive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM857244 503 bp mRNA linear EST 06-MAR-2002 K-EST0141477 S21SNU520 Homo sapiens cDNA clone S21SNU520-78-F09 5', mRNA sequence.
BM857244
                             EST 29-JAN-1999
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J. W., Park, H.S., Kim, S. and
                      qm62c06.x1 Soares placenta_8to9weeks_2NbHp8to9W Homo sapiens cDNA clone IMAGE:1893322 3' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS AISHORA RLLX.; , mRNA sequence.
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 503)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1323 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 440.
Location/Qualifiers
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100.0%; Pred. No. 5.7e+02;
ive 0; Mismatches 0; Indels
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21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1893322"
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                                                                                                          AI283063.1 GI:3921296
                                                                                                                                           sapiens (human)
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//one libe #8218NUS20"
//one #8218NUS2
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1 (bases 1 to 542)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu.,C., Fang,R., Guegler,R., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton.L.M.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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17000424524143 GRN_EB Homo saplens cDNA 5', mRNA sequence.
CN422262
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Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Sz Ecoun-dongy Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 78 row: F column: 09
High quality sequence stop: 503.
Location/Qualifiers
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Fai: 650 473 7760
Email: rbrandenberger@geron.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell type="Floating aggregates"
|cell_line="SNU-520"
|lab_host="Topl0F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="S21SNU520-78-F09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/daw stage="Adult"
//dab_host="Adult"
//dab_host="EMDH10B"
//dlobe lib="Human Lens cDNA (Normalized): fs"
//dlobe lib="Human Lens cDNA (Normalized): fs"
//dlobe lib="Human Lens cDNA (Normalized): fs"
//note="Organ: Bye; Vector: DCMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by Not! This Not! digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (life
Technologies). Single-stranded DNA (1 mg) was hybridized
(COt 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases I to 560) Wistow, G., Bernstein, S.L., Wyatt, M.K., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of adult human lens for the NEIBank Project: over 2000 non-redundant transcripts, novel genes and splice variants
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UI-HF-PQO-aws-e-16-0-UI.rl NIH_WGC_215 Homo sapiens cDNA clone
CP131978
                                                                  fa25h07.yl Human Lens CDNA (Normalized): fs Homo sapiens cDNA clone fa25h07.yl mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: graeme@helix.nih.gov
Plate: 25 row: h column: 07
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .560
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                        /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_lib="GRN_BB" /note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular denome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de,
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp686N10257) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERNANY; Email: clone@rzpd.de.
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Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and Wiemann,S.
Erg (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
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/note="vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
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Std Error: 0.00
                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZp686N10257"
                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
Length: 542 Std Erro
Location/Qualifiers
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Search completed: February 5, 2005, 08:11:42 Job time : 2151.2 secs
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                                                   Contact: MIPS
           Wiemann, S.)
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/clone="INMGE:3053743"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="Unit MGC 215"
/clone_lib="NIH MGC 215"
/clone_lib="NIH MGC 215"
/note="Organ: Lung; Vector: pXX-Asc; Site_l: EcoR I;
Site_2: NOT I; The library was constructed accordings
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand CDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 58)
Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 57). Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                               375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
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                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Mary Hendrix
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                                               Homo sapiens (human)
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Heidelberg/Germany) within the cDNA sequencing consortium of the
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Canc
Research Center (DREZ), Email s.Wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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0
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This clone (DKFZp547K2090) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 584;
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/lab_host="X1-2blue"
/clone_lib="547 (synonym: hfbr1)"
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ilarity 100.0%; Pred. No. 5.9e+02;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="DKFZp547K2090"
                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="brain"
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100.0 702 6 BD102202 100.0 702 9 BT007208 100.0 702 12 BT08248 100.0 737 9 HSU72398	18 100.0 737 6 18 100.0 737 6	18 100.0 737 6 AR360913 18 100.0 737 9 HSPCLXS	18 100.0 926 6 18 100.0 926 6 18 100.0 926 6 18 100.0 926 6 18 100.0 926 6 18 18 100.0 926 6 18 18 100.0 926 6 18 18 100.0 926 6 18 18 100.0 926 6 18 18 18 18 18 18 18 18 18 18 18 18 18	18 100.0 926 6 AR144311 18 100.0 926 6 AR172594 18 100.0 926 6 BD243042	18 100.0 926 6 CQ765842 CQ7658 18 100.0 926 6 E58777 E59777 E59777 152011	18 100.0 926 6 AR371661	18 100.0 926 6 AX839772 AX839772 Sequence 18 100.0 926 6 AX83972 AX838772 Sequence 18 100.0 926 6 AX8387686 AX825686 AX825686 Sequence	18 100.0 1236 6 AXO85490	ALIGNMENTS	z		_	AUTHORS Stein, C.A. TITLE Oligonalectide inhibitors of bcl-xL		FU 02-001-2002 PF 02-001-1999 JP 2000557839 PR 02-001-1998 US 09/109614 PI CY A STEIN	PC C12N15/09, A61K9/127, A61K9/51, A61K31/711, A61K31/712, A61K31/7125, PC	A61K47/42, PC A61K47/48, A61K48/00, A61P35/00, C12N15/00 CC ANTISENSE OLIGONUCLEOTIDE FH Key T source 1 .18	Location/Qualis 1. 18 /organism="synt/mol_type="genc/mol_type="gen		Query Match 100.0%; Score 18; DB 6; Length 18; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 CTTTACTGCCATGGG 18
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5.1.6 Compugen Ltd.	roh time 432 664 Seconda					9053458								l by chance to have a the result being printed, e distribution.		ţį	00000	CQ185831 Sequence CQ235904 Sequence CQ2734777 Sequence CQ310858 Sequence	CQ100639 Sequence CQ139631 Sequence	, 0, 0, 0, 0	CO333104 Sequence BD097037 A BH4 fue BD084108 Method of
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compu	rch, using sw model		-09-753-169A-6 ctttactgctgccatggg 18	IDENTITY NUC Gapop 10.0 , Gapext 1.0	29 seqs, 23644849745 residues	satisfying chosen parameters:	t: 0 :: 200000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	b]:*	gp_ba:* gb_htg:* gb_in:* gb_on:* gb_ov:*	h_pat:* h_ph:* b_pl:*	9b_pr:* 9b_ro:* 9b_sts:*	gb_sy:* gb_un:* gb_vi:*	the number of results predicted by chance to have r than or equal to the score of the result being pied by analysis of the total score distribution.	SUMMARIES	Length DB ID	18 6 18 6 512 6 555 6	555 6 CQ185831 555 6 CQ235904 555 6 CQ273477 555 6 CQ37773	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	9 9 9 9	636
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LOCUS DEFINITION ACCESSION VERSION

RESULT 2 BD235170

KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL REFERENCE

COMMENT

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1. :555

/organism="Homo sapiens"

/mol type="unassigned DNA"

/mol type="taxon:960"

/mol type="taxon:960"

/mol type="taxon:960"

/note="MAP TO All17381.9~EXPRESSED IN PLACENTA, SIGNAL = 0.99~SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                                                                                                                                                                                                                                       Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 22554 09-AUG-2001;
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     Sequence 13703 from Patent WO02068579
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CQ113695.1 GI:41083565
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                              CQ727769.1 GI:42294740
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Oligomucleotide inhibitors of bcl-xL
Oligomucleotide inhibitors of bcl-xL
Patent: JP 2002519048-A 22 02-JUL-2002;
Patent: Groupward University in THE CITY OF NEW YORK
OS Artificial Sequence
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100.0%; Pred. No. 2.3e+02;
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02-JUL-1998 US 09/109614
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/db_xref="taxon:32630"
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BD235170.1 GI:33044940
JP 2002519048-A/22.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_txef="taxon:5606"
/note="MAP_TO_AL117381.9~EXPRESSED IN FETAL_LIVER, SIGNAL
= 3.5-SWISSEROT_HIT: Q07817, EVALUE 1.00e-106~EST_HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT_HIT: U72398.1, EVALUE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
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iive 0; Mismatches 0;
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CQ273477
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/organism="Homo
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                                                                                      Homo sapiens (human)
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/db xref="teaxon.9606"
/noTe="wAP TO ALIL1301.9-EXPRESSED IN BONE MARROW, SIGNAL
/noTe="wAP TO ALIL1301.9-EXPRESSED IN 00-106-EST HUMAN
= 4.7-SWISSPROT HIT: 007817, EVALUE 1.00e-106-EST HUMAN
HIT: BEZ07063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                                                                                                               Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart
Patent: WO 0157274-A 17227 09-AUG-2001;
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                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutel:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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     GI:41159924
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/db_xref="taxon:9606"
/note="MAP_TO AL117381.9~EXPRESSED IN BONE MARROW, SIGNAL
= 4.7"
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
1. 600
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db xref="taxon:9606"
/noce="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 9653 09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                              probes useful
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                         Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid analysis of gene expression in human placenta Patent: WO 015/272-A 9498 09-AUG-2001;
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Sequence 9653 from Patent WO0157276.
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Location/Qualifiers
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/organism="Homo sapiens"
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       CTTTACTGCTGCCATGGG 18
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CQ100639.1 GI:41069665
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CQ139631.1 GI:41097003
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CQ139631
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN BRAIN, SIGNAL = 1.6~SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN HIT: BE207063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE
0.00e+00"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="teaxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN LUNG, SIGNAL =
Z~SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN HIT:
BEZ07063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE
0.00e+00"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid analysis of gene expression in human lung Patent: WO 0186003-A 21963 15-NOV-2001; Aeomica, Inc. (US)
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Sequence 21867 from Patent WO0157275.
CQ347773
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Sequence 21963 from Patent WO0186003.
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/organism="Homo sapiens"
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Location/Qualifiers
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CTTTACTGCTGCCATGGG 321
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Matches 18; Conservative
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/db_xref="reacn:9606"

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= 1.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER-130- PB 0004 WO
3<150- US 60/106/312-151- O4 February 2000 (04.02.00)<150- US
60/207, 456<151- 26 May 2000 (26.05.00)<150- US 09/632,366<151- O3
4049442 2000 (03.08.00)<150- US 60/236,359-151- O3 October 2000
(27.09.00)<150- US 60/234,687-151- 27 September 2000
(21.09.00)<150- US 69/234,687-151- 21 September 2000
(21.09.00)<150- US 09/608,408<151- 30 June 2000 (30.06.00)<170-
Molecular Dynamics Sequence Listing Engine
Patent: WO 0157273-A 9838 09-AUG-2001;
Aeomica, Inc. (US)
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                         Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
Patent: WO 0157274-7 360 09-AUG-2001;
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;

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                                                               Sequence 7360 from Patent W00157274.
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Location/Qualifiers
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/db xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN FETAL LIVER, SIGNAL
= 3.5"
                                                                                                                                                                                                                                                                                                Euteleostomi;
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human fetal liver

Patent: WO 015277-A 9222 09-AUG-2001;

Acomica, Inc. (US)

Location/Qualifiers
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Sequence 9222 from Patent WO0157277.
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us-09-753-169a-6.rng

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ı Ltd.		; Search time 232.23 Seconds (without alignments) 406.880 Million cell updates/sec				8269772			
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: February 4, 2005, 15:50:53 ; Search (without a 406.880 Mi	Title: US-09-753-169A-6 Perfect score: 18 Sequence: 1 ctttactgctgccatggg 18	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 4134886 segs, 2624710521 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : N Geneseq 23Sep04:* 1:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz46976 Bcl-X1 mR	Aba73433 Human foe	Aai53868 Probe #22	Aba38761 Probe #17	Aak48039 Human bon	Aak21876 Human bra	Abs47753 Human liv	Abs21972 Human gen	Ach87595 Human gen	Aba60917 Human foe	Aai40812 Probe #94	Aba28894 Probe #73	Aak35096 Human bon	Aak09207 Human bra	Abs34848 Human liv	Abs09558 Human gen	Aah48169 Mutant bc	Aah43464 cDNA clon	Adm45994 Human apo	Aag81699 Human thy	Abz83507 Toxicolog
SUMMARIES	QI	AAZ46976	ABA73433	AA153868	ABA38761	AAK48039	AAK21876	ABS47753	ABS21972	2 ACH87595	ABA60917	AA140812	ABA28894	AAK35096	AAK09207	ABS34848	ABS09558	AAH48169	AAH43464	2 ADM45994	AAQ81699	0 ABZ83507
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Probe #22554 used to measure gene expression in human placenta sample.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
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                                                      AAI53868 standard; DNA; 555
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 lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpyridyl)porphine and/or tetra meso-(antihiuw)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-X1 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 21738; 639pp + Sequence Listing; English.
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                                                                                            100.0%; Score 18; DB 3; Length 18; 100.0%; Pred. No. 20;
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                                                                   Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408,
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Best Local Similarity 100.0%;
Matches 18; Conservative (
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                                                                                                                                                                          crirracrecreccarese
                                                                                                                                                                                                                                            ABA73433 standard; DNA; 555
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                                                                                        Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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8888888
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2000US-0180312P

(first entry)

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #17227 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                          Claim 25; SEQ ID NO 22554; 654pp; English.
                                             DR;
                                             Rank
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(MOLE-) MOLECULAR DYNAMICS INC
                                             Chen W,
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1es 18; Conservative
                                             Hanzel DK,
                                                                                      WPI; 2001-488897/53
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                                             Penn SG,
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Gaps

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Mismatches

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CTTTACTGCTGCCATGGG 321

304

CTTTACTGCTGCCATGGG 18

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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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                                                                                                                                               Rank DR;
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                                                                                                                                                                                                                                           gene expression in human bone marrow
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                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                 Chen W,
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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2000US-00608408
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Best Local Similarity, 100.
Matches 18, Conservative
                                                                                                                                               Hanzel DK,
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21-SEP-2000;
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microcarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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                                                                                                                                             2000US-0180312P.
2000US-0207456P.
2000US-00608408.
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26-MAY-2000; 2000US-0207456P.
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                                  WO200157274-A2.
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03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
 sapiens
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Matches

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AAK48039 ID AAK4

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Gaps

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0; Indels

4; Length 555;

Gaps

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0; Indels

4; Length 555;

DB ,

100.0%; Score 18; DB 100.0%; Pred. No. 30; ive 0; Mismatches

BP.

(first entry)

G; 133 T; 0 U; 0 Other;

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liver single exon nucleic acid probes of the invention. Note: The agequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicortosis; lymphangioleiomyomicosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary bypertension; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
                                                                                                      Seguence 555 BP; 105 A; 178 C; 139
                                                                                                                                                                                                                                                                          304 CTTTACTGCTGCCATGGG 321
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                              probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                   Gaps
                                                             The present invention provides a number of single exon nucleic acid
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hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
                     4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                          100.0%; Score 18; DB 4; Length 555; 100.0%; Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                   0; Mismatches
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2000US-00608408.
2000US-00632366.
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Les 18; Conservative
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                       invention
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                                                                                                                                                                                                                                                                                                                   Matches
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising ele expression in a sample collection of detectably labeled nucleic acids derived from human lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 21963; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000665.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
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                                                               WO200186003-A2
Homo sapiens.
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                                                                                                                                   15-NOV-2001
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Target, identifying exons in a eukaryotic genome, comparising (a) algorithmically predicting at least one exon from genomic sequences of algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included to in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the expression of the exons in the specification, or encoded by the cyrobes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene; particularly using human correr, chronic obstructive pulmonary diseases (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease. Hermansky-correspondences, mentioned by pulmonary dysplasia, primary ciliary dyskinesis, pulmonary haemosisderosis, pulmonary probes open reading frame of the prime syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskines specification, but was obtained in electronic format directly formation. Note: The sequence data for this patent did not form part of remembrance of the prime and the contraction and hyaline membrane disease.
   measuring the label detectably bound to each probe of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the printed specification, but was obtained in electro from WIPO at ftp.wipo.int/pub/published_pct_sequences
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100.0%; Score 18; DB 6; Length 555; Indels ; 0 30; 0; Mismatches Pred. No 321 1 CTTTACTGCTGCCATGGG 18 100.08; 304 crrracrecreccarees Query Match 100. Best Local Similarity 100. Matches 18; Conservative ò 셤

Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

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ACH87595 standard; DNA; 564 BP. 29-JUL-2004 ACH87595; RESULT 9 ACH87595

Human genome derived single exon probe #20790. (first entry)

Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.

Homo sapiens

US2003194704-A1 16-0CT-2003. 03-APR-2002; 2002US-00029386

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Rank DR, Hanzel DK; Penn SG,

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative

methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human patent did not form part of the priming the sequence data for this patent did not form part of the primited sequence data for this The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleocide acquences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a wector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid substitutions), an expense of stolated antibody that binds specifically to a peptide cited above, ö Gaps for assessing genomic alterations or as tools for ÷ 100.0%; Score 18; DB 12; Length 564; 100.0%; Pred. No. 30; cive 0; Mismatches 0; Indels (Sequence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other; segdata.uspto.gov/seguence.html?DocID=20030194704 Claim 1; SEQ ID NO 20790; 80pp; English. Conservative Local Similarity es 18; Conserv surveying tissues. splicing events, Query Match Matches

1 CTTTACTGCTGCCATGGG 18

CTTTACTGCTGCCATGGG 321 304

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ABA60917;

ВЪ.

ABA60917 standard; DNA; 600

RESULT 10

ABA60917

Human foetal liver single exon nucleic acid probe #9222. (first entry) 01-FEB-2002

Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

Homo sapiens

WO200157277-A2

09-AUG-2001.

30-JAN-2001; 2001WO-US000669

04-FEB-2000; 2000US-0180312P

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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO
                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                              100.0%; Score 18; DB 4; Length 600; 100.0%; Pred. No. 30;
                                                                                                                                                    Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
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                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                    Chen W,
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                03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408.
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2000US-0234687P
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Best Local Similarity 100.
                                                                                    Penn SG, Hanzel DK,
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                                                                                                       WPI; 2001-483447/52
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                             04-OCT-2000;
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30-JUN-2000;
         30-JUN-2000;
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                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                  Claim 25; SEQ ID NO 9498; 654pp; English
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gene expression in human placenta.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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nes 18; Conservative
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SXS

AAK35096;

RESULT 1:

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Human, brain expressed exon, gene expression analysis; probe, microarray, Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
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hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
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                                                                                                    Human brain expressed single exon probe SEQ ID NO: 9198.
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     ВЪ.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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   AAK09207 standard; DNA; 600
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                                                                    (first entry)
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nes 18; Conserv
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                                                                                                                                                                                                          Homo sapiens.
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30-JUN-2000;
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                                   AAK09207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed single exon probe SEQ ID NO: 9653.
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                                                                     Length 600;
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                                Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
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Pred. No. 30;
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                                                                  ch 100.0%;
l Similarity 100.0%;
18; Conservative 0;
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2000US-0236359P
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Matches 18; Conservative
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27-SEP-2000;
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30-JUN-2000;
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coronary heart disease; ss.

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Homo sapiens

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed sepecification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 18; DB 4; Length 600;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 9838; 658pp; English.
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                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                         26-MX-2000; 2000US-0207456P.
30-UIN-2000; 2000US-0060B40B.
03-MG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0236359P.
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                                                                                                                                          2000US-0180312P
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                    WO200157273-A2
                                                            09-AUG-2001
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Gaps ö

Search completed: February 4, 2005, 21:52:42 Job time : 232.23 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	C 26	18 100.0
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Searched: 32822875 segs, 18219865908 residues		
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Maximum Match 100%	RESULT 1	
Listing lirst 45 summaries	BE818726/c	20101010
Database : EST:*	DEFINITION	PM3-BN0300-
	ACCESSION	BE818726
	VERSION KEYWORDS	BE818726.1 EST.
4: gb_est3:*	SOURCE	Homo sapien
	ORGANISM	Homo sapien
6: gb_est5:* 7: gb_est6:*		Eukaryota; 1
	REFERENCE	1 (bases 1
	AUTHORS	Dias Neto, E

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	BE818726	BE818722	BI060608	BI045645	AZ576742	BM844286	CF145335	AZ537061	CN422261	BQ331598	BG746308	BM857244	H09884 ym05b07.rl	CN422262	CD675630	CF131978	AL134785	BE871836	AW732926	BE783664	BF038769	CF131456	CN422264	BI489889
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SUMMARIES	8	BE818726	BE818722	BI060608	BI045645	AZ576742	BM844286	CF145335	AZ537061	CN422261	8Q331598	BG746308	BM857244	H09884	CN422262	CD675630	CF131978	AL134785	3E871836	AW732926	BE783664	BF038769	CF131456	CN422264	81489889
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM3-BN0300-080
700-002-glikt3=2000-07-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 33
High quality sequence stop: 294.
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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PM3-BN0300-080700-002-g11 BN0300 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 294)

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                 low stringency conditions."
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0300"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
/do_vrege="Adult"
/clone lib="Urgun: uterus tumor; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
No. 196, 716 - Dudwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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1 (bases 1 to 3 arcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Garcalho, A.F., Warjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bará, G.S., Simpson, D.H., Matstein, A., deoliveire, P.S., Matchen, P.S., Gorges, F., Carvalho, A.F., Matchen, G.S., Gimpson, D.H., O'Harre, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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MR3-FN0206-300101-004-h07 FN0206 Homo sapiens cDNA, mRNA sequence.
BI045645
                                                                                                                                                                                        BI060608 310 bp mRNA linear EST 15-JUN-2001 IL3-UT0115-300101-433-B03 UT0115 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpsonebludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0115-
300101-433-B03&t3=2001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
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100.0%; Score 18; DB 2; Length 294; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels

Local Similarity 100.

Best Loc Matches

Query Match

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/organism="Homo sapiens"
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                                                                  Gene Expression
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BM844286
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                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 317)

1 blas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Rogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/soripts/gethtml2.pl?tl=MR3&t2=MR3-FN0206-
300101_004-h07&t3=2001-01-30&t4=1)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 34.
Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M.,
Bernardino, A., Durick, K. and Pollok, B.
                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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/clone lib="FN0206"
/note="Grgan: prostate_normal; Vector: puc18; Site_1:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
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AST-2T00919 Genetrap T47D Human Breast Carcinoma Library Homo
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/mol_type="mRNA"
/db_xref="taxon:9606"
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High quality sequence stop: 317,
Locarion/Qualifiers
1..317
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  GI:14452267
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                                            Homo sapiens (human)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
(bases 1 to 421)
(bh.W.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',
                                                                                                                                                                                                                               Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter dilying neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmpl and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library"
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Korea Research Institute of Bioscience & Biotechnology
52 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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Exon-trap tags from a T47D GenomeScreen(TM) Library
                                                                                                                                                       USA
                                                                                                                                                    CA 92121,
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Unpublished (2002)
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/cell type="Epithelial"
/cell line="T47D"
                                                                                                               Aurora Biosciences Corp.
11010 Torrevana Road, San Diego,
Tel: 8584046419
Pax: 8584046719
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Plate: 63 row: B column: 03
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                           Contact: Greg Henkel
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/note="Organ: Prostate; Vector: pAmp-1; 3' RACE of total
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Gene Expression
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Matches 18; Conservative
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                                                                                                                                                                                                                 /deal_line="XNU-216"
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/clone_lib="Stored"
/clone_lib="S
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Email: bento-soares@uiowa.edu
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100.0%; Pred. No. 2.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                 /tissue_type="Lymph node"
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Genome Res. 6 (9), 791-806 (1996)
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18; Conservative 0
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11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584046413
Fax: 85840464719
Email: henkelg@aurorabio.com
Pools of cells ware isolated from a GenomeScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DHS-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
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AST-2P01514.AB Genetrap PC-3 Human Prostatic Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
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Exon-trap tags from a PC-3 GenomeScreen(TM) Library Unpublished (2000)
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us-09-753-169a-6.rst

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Homo sapiens (human)
                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
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/note="oligo dT_primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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BQ331598
BQ31598.1 GI:20972765
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
RNA from genetrap pools; shotgun clone in pAmp-1 and to transform DH5-alpha competent bacteria."
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derived_from H1, H7 and H9 cells"
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17000424524125 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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                                                               ch 100.0%; Score 18; DB 8; L
l Similarity 100.0%; Pred. No. 2.4e+02;
18; Conservative 0; Mismatches 0;
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Insert Length: 474 Std Error: 0.00.
Location/Qualifiers
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Matches 18; Conserv
                                                                               Best Local Similarity
Matches 18; Conserv
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
1 (bases 1 to 475)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
G'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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602703549F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856725 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry ab be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ET0138-080501-010-d06&t3=2001-05-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 41
High quality sequence start: 41
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/organism="Homo sapiens"
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/UGULTURE TOWN DEALESTS // CLORE "INRAME: 4856725" // CLORE "INRAME: 4856725" // CLORE "INRAME: 4856725" // CLORE "INRAME: 4866725" // CLORE TYPE "adenocarcinoma cell line" // Lissue Lype "adenocarcinoma cell line" // Lissue Lype "adenocarcinoma cell line" // Clore libe"NIH MGC 15" // Nector: POTB7; Site 1: XhoI; Site 2: // Nece "Organ: colored yo oligo-dT priming. Directionally clored into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov.blate: Lcage.lln.gov column: 14 Plate: Lcage.lln.gov.a column: 14 High quality sequence stop: 464.
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Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 78 row: F column: 09
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
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/cell_type="Floating aggregates"
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                                                                                                                                                                                                  /organism="Homo sapiens"
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/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: ECORI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toploff' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
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1 (Dass 1 to 516)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulenn,M., Kucaba,T., Le,M., Lenno,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
Insert Size: 1997
High quality sequence stops: 249
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1997 Std Error: 0.00
Seq primer: MISRP1
High quality sequence stop: 249.
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Unpublished (1995)
Unpublished (1995)
Unpublished (1995)
Washington University School of Medicine
Washington Purk Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 503;
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
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Homo sapiens
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Loca 18; Conserve
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Search completed: February 5, 2005, 08:11:44
Job time: 2148.2 secs
      Es25h07 5', mRNA sequence.
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22103463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger.
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 542)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
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7000424524143 GRN_EB Homo sapiens.CDNA 5', mRNA sequence
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                                                                                                                                                             100.0%; Score 18; DB 7; Length 516; 100.0%; Pred. No. 2.5e+02;
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Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rbrandenberger@geron.com
Insert Length: 542 Std Error: 0.00.
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Geron Corporation
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Best Local Similarity 100.7
Marches 18, Conservative
                                                                                                                                                                                          18; Conservative
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CN422262/c
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CD675630/c
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/clone libe-"Human Lens cDNA (Normalized): fs"
/clone libe-"Human Lens cDNA (Normalized): fs"
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid bNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(COT SOO) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
                                                                                                                                                                                                                                                           Wistow, G., Bernstein, S.L., Wyatt, M.K., Behal, A., Touchman, J.W.,
Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 560)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Section on Molecular Structure and Function National Bye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 25 row:h column: 07 Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Vis. 8 (4), 171-184 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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/lab_host="EMDH10B"
CD675630
CD675630.1 GI:32177361
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                                                                                              Homo sapiens (human)
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AX525912 Sequence X83574 M.musculus

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Sequence:

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Title:

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U34963 Rattus norv
876513 bcl-x=apopt
AX127122 Squence
AU001203 Sus scrof
U10579 Rattus norv
AF16517 Ovis arie
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AR118504 Sequence
AR14311 Sequence
AR14311 Sequence
AR172594 Squence
BD243042 Antisense
CQ765842 Sequence
BD243042 Antisense
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BD243042 Antisense
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ES8777 Screening m
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BD102202 Method fo
BT007208 Homo sapi
U10101 Mus musculu
                                                                        BT008248 Synthetic
AF216205 Sus scrof
U72398 Human Bcl-x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonuclectide inhibitors of bcl-xL
Patent: JP 2002519048-A 7 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/7
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                                                                                                                                                                                                                                                                                                                                                                                                               linear
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C A61K47/48,A61K48/00,A61P35/00,C12N15/00
C ANTISENSE OLIGONUCLEOTIDE
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AX127722
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02-JUL-1998 US 09/1096:
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BD243042
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BD235155.1 GI:33044925
JP 2002519048-A/7.
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1967.381 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 4526729 seqs, 23644849745 residues
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Maximum Match 100%
Listing first 45 summaries
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PAT 17-JUL-2003

Gaps

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AR371661 Sequence

Minimum DB Maximum DB

Database

Result g

Searched:

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                               AF245487 541 bp mRNA linear MAM 11-APR-2001
Bos taurus clone 1.1 anti-apoptotic regulator Bcl-xL mRNA, partial
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Bos taurus clone 1.2 anti-apoptotic regulator Bcl-xL mRNA, partial
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Amills,M. and Bouzat,J.
Characterization of the bovine bcl-xL gene and related pseudogenes
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Amills,M. and Bouzat,J.
Characterization of the bovine bcl-xL gene and related pseudogenes
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Bovinae; Bos.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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Submitted (15-MAR-2000) Unitat de Genetica, Facultat de
Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B.,
Bellaterra Barcelona 08193, Spain
Location/Qualifiers
1. 541
/organism="Bos taurus"
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2 (bases 1 to 541)
Amills,M. and Bouzat,J.
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Amills, M. and Bouzat, J.
                                                                                                                                 AF245487.1 GI:13591635
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stent: JP 2002519044-A 23 02-UUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
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                                                                                                                                            ON Oligonucleotide inhibitors of bcl-xL.

M BD235171

M BD235171

M BD235171.1 GI:33044941

M P 2002519048-A/23.

Synthetic construct

M synthetic construct

artificial sequences.

I (bases 1 to 20)

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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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02-JUL-1999 JP 2000557839
02-JUL-1998 US 09/109614
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PAT 21-JAN-2004
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/mol_type="taxon:9606"
/db xref="taxon:9606"
/nofe="whap TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL = 0.99-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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/db_xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN BONE MARROW, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                = 4.7-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT: B2207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE 0.00e+00.
                                                                                                                                                          Euteleostomi;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 015/7272-A 22554 09-AUG-2001;
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 22596 09-AUG-2001;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                  CO113695 DNA Sequence 22554 from Patent WO0157272.
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Sequence 22596 from Patent WO0157276.
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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Location/Qualifiers
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BEBERAKRAFSBLTSQLHITPGTAYQSFEQVVNBLFRDGVNWGRIVAFFSFGGALCV
ESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQBRF
NRWFLTGMTYNGVVLLGSLF"
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ESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERF
NRWFLTGMTVAGVVLLGSLF"
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Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial
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Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (15-MAR-2000) Unitat de Genetica, Facultat de
Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B.,
Bellaterra, Barcelona 08193, Spain
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                                                                                                   product="anti-apoptotic regulator Bcl-xL"
protein_id="AAK31307.1"
db_xref="GI:13591638"
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/protein_id="AAK31308.1"
/db_xref="GI:13591640"
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100.0%; Pred. No. :
ive 0; Mismatch
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Pred. No.
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   taurus"
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'mol_type="mRNA"
'db_xref="taxon:9913"
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/codon_start=1
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AF245489.1 GI:13591639
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Matches 20; Conser
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HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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BE202063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE
0.00e+00"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human fetal liver
Patent: WO 0157277-A 21738 09-AUG-2001;
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        Length 555;
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     DB
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CQ310858.1 GI:41271435
     100.0%;
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/mol_type="unassigned DNA"

/db_xref="texcon:9606"

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HE207063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE

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HUMAN GENOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER-130- PB 0004 WO 3<br/>
3<br/>
4.150- US 60/180, 312-4151- 04 February 2000 (04.02.00)<br/>
4.56-6115- 26 May 2000 (26.05.00)<br/>
4.56-6115- 26 May 2000 (26.05.00)<br/>
4.50-00 (03.08.00)<br/>
4.50-00 (03.08.00)<br/>
4.50-00 General September 2000 (27.09.00)<br/>
4.50-00 (03.09.00)<br/>
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0157274-A 17227 09-AUG-2001;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Sequence 17227 from Patent WO0157274.
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PAT 21-JAN-2004
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| organism="Homo sapiens"
| /organism="Homo sapiens"
| mol_type="unassigned DNA"
| db_xref="taxon:9606"
| / db_xref="map TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL
= 4.7"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0152274-A 7360 09-AUG-2001;
Aeomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
patent: WO 0157276-A 9653 09-AUG-2001;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 9653 from Patent WO0157276.
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Sequence 7360 from Patent WO0157274.
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="WAP TO AL117381.9~EXPRESSED IN PLACENTA, SIGNAL
/.ope="Amagna To AL117381.9
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 9498 09-AUG-2001;
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human brain
Patent: WO 0157275-A 21867 09-AUG-2001;
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Sequence 9498 from Patent WO0157272.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz46977 Bcl-Xl mR '	Adk66037 Standardi	Ach46093 Human inf	Aba73433 Human foe	Aai53868 Probe #22	Aba38761 Probe #17	Aak48039 Human bon	Aak21876 Human bra	Abs47753 Human liv	Abs21972 Human gen	Ach87595 Human gen	Aba60917 Human foe	Aai40812 Probe #94	Aba28894 Probe #73	Aak35096 Human bon	Aak09207 Human bra	Abs34848 Human liv	Abs09558 Human gen	Aah48169 Mutant bc	Abt09346 Phase-1 R	Aah43464 cDNA clon
SUMMARIES	ΩΙ	AAZ46977) ADK66037	ACH46093	ABA73433	AAI53868	ABA38761	AAK48039	AAK21876	ABS47753	ABS21972	2 ACH87595	ABA60917	AAI40812	ABA28894	AAK35096	AAK09207	ABS34848	ABS09558	AAH48169	ABT09346	AAH43464
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Add55218 Human apo Ad552218 Human Bcl Ad55209 Human Bcl Ad516926 Human Bcl Ad41699 Bcl-xL ge Ad29816 Bcl-xL ge Ad29816 Human bcl Ad2981189 Human bcl Abk84766 Human Bcl Abk84766 Human Bcl Ad65779 Human bcl Ad45779 Human bcl Ad452630 Human bcl Ad4132104 Human bcl Ad4132104 Human cDN Ad4132104 Human cDN Ad413218 Renal ccl Ad013990 Human RCN Ad013951 Renal ccl Ad013951 Renal ccl Ad081375 Bcl-xl-DT Ad085177 Bcl-xl-DT Ad085177 Parnesyl Ad685177 Parnesyl Ad685177 Parnesyl Ad685177 Parnesyl Ad685177 Parnesyl Ad685177 Parnesyl Ad685177 Parnesyl Ad685177 Parnesyl	SINS					; cancer; epithelial; prostate; antisense; ss.				•					ing the anti-apoptotic protein bcl- ion in tumor cells to treat cancer gression of vascular lesions.		invention provides antisense oligonucleotides or their derivatives in reduce or eliminate expression of the anti-apoptotic protein bcl. The oligonucleotides can be introduced into tumour cells to reduce state, lung or bladder cancer. Sepecially epithelial cancer, e.g. state, lung or bladder cancer. Oligonucleotides comprising one or more swith a C-5 propynyl pyrimidine modification may especially be used reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in treatment. The oligonucleotides can be introduced into vascular is to reduce bcl-xL production to promote the regression of vascular
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Human; se; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

Human infant brain cDNA #156.

US2003073623-A1 Homo sapiens

13-OCT-2003 (first entry)

ACH46093;

156 CGCCGTTCTCCTGGATCCAA 137

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ACH46093 standard; cDNA; 492 BP

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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-Xl mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; standardized polynucleotide system; medical diagnosis; functional genomics; sample analysis.
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                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is a polynucleotide used in the system of the invention
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                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 7.4; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Standardized polynucleotide system polynucleotide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
                                                                                                                                                                                             Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCGTTCTCCTGGATCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2002; 2002DE-01009071
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Best Local Similarity 100.0
Matches 20, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK66037;
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ID ADK6603
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           8X33333
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polyneptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are asful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obtained in electronic format directly from USPTO segdata.uspto.gov/seguence.html?DocID=20030073623
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Matches 20, Conservative
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STACHE-CRAIN F
DICKSON M C.
JONES L W.
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100.0%; Score 20; DB 10; Length 337; 100.0%; Pred. No. 9.1; tive 0; Mismatches 0; Indels (

100.0%; Fr.

Local Similarity 100.

Matches

Query Match

1 CGCCGTTCTCCTGGATCCAA 20

ABA73433

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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #17227 for gene expression analysis in human heart cell sample.
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cardiovascular disease, hypertension, cardiac arrhythmia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 4; Length 555;
Pred. No. 9.4;
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                                                                                                                                                                                                                                                                                                                                                                   gene expression in human placenta.
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                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                    2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                  30-JAN-2001; 2001WO-US000663
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Conservative (
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2000US-0236359P.
2000GB-00024263.
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Best Local Similarity
Matches 20; Conserv
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WO200157272-A2
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                                                                                                                     26-MAY-2000;
30-JUN-2000;
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                              09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                  Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used to measure gene expression in human placenta sample.
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                                                                                                               Human foetal liver single exon nucleic acid probe #21738.
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                                                                                                                                                                                                                                                                                                                                               2000US-0207456P.
2000US-00608408
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21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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              ABA73433 standard; DNA; 555
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nes 20; Conserv
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30-JUN-2000;
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                                                                               01-FEB-2002
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Matches
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RESULT 5

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Gaps

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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays by measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                    Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                            present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                   Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                               Claim 4; SEQ ID NO 17227; 530pp; English
              DR;
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             Rank
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              Chen W,
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2000US-0236359P
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              Hanzel DK,
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                                        WPI; 2001-488899/53
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27-SEP-2000;
04-OCT-2000;
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             probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes which are derived from genomic sequences expressed in the human brain. They can be used from genomic sequences expressed in the human which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                      such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
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present invention provides a number of single exon nucleic acid
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                                                                                                                                               Length 555;
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                                                                                                            Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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                                                                                                                                            100.0%; Score 20; DB 4;
100.0%; Pred. No. 9.4;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632468.
21-SEP-2000; 2000US-0234687P.
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Best Local Similarity
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Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomcosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.

Human genome-derived single exon probe ORF from lung SEQ ID No 21963.

BP.

ABS21972 standard; DNA; 555

19-AUG-2002 (first entry)

ABS21972;

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements / fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABSESO11-ABSES1005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed for a single action but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                         Human, single exon nucleic acid probe, liver, cirrhosis,
hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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21-SBP-2000; 2000US-0234687P.
-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000CB-00024263.
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2000US-00608408
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                                                                                                                  ABS47753 standard; DNA; 555
                                                                                                                                                                                                                                                                                             coronary heart disease, ss.
                                                                                                                                                                                        (first entry)
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ABS47753
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Rank DR;

Chen W,

Hanzel DK,

Penn SG,

WPI; 2002-114183/15

(MOLE-) MOLECULAR DYNAMICS INC.

26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-00608408. 03-MUG-2000; 2000US-00632466. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-023559P. 04-OCT-2000; 2000GB-00024263.

30-JAN-2001; 2001WO-US000665

34-FEB-2000;

WO200186003-A2 Homo sapiens

15-NOV-2001

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The invention relaters to a spatially-addressable set to a single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung cacid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 perobes. Also included are a microarray comprising the novel set of probes of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; measuring gene expression in a sample carid expressed in the human lung; measuring gene expression in a sample carid expressed in the human lung; measuring the jabel detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) conjection of detectably predicting at least one exon from genomic sequences of the eukaryote; and (b) measuring at least one exon from genomic sequences of algorithmically predicting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single gene, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon and expression of the exons should be assigned to a single gene; a peptide comprising one expression fervances, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression canalysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon
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Gaps ö

ch 100.0%; Score 20; DB 4; Length 555; 1 Similarity 100.0%; Pred. No. 9.4; 20; Conservative 0; Mismatches 0; Indels

Best Local Similarity

Query Match Matches 1 CGCCGTTCTCCTGGATCCAA 20

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cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tubercus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histlocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Matches 20, Conservative
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     8XGGGGGGGGGGG
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Human genome derived single exon probe #20790. 1 CGCCGTTCTCCTGGATCCAA 20 ACH87595 standard; DNA; 564 BP. (first entry) 29-JUL-2004 ACH87595; RESULT 11 ACH87595 ò g

Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.

Homo sapiens

16-OCT-2003

US2003194704-A1

03-APR-2002; 2002US-00029386

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK,

WPI; 2004-119264/12

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 1; SEQ ID NO 20790; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of

Claim 1; SEQ ID NO 9222; 639pp + Sequence Listing; English

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measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing than gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the probes may be used as tools for surveying tissues to detect the presence of expressed measages that contain their specific exon, or in constructing genome-edrived single exon microarrays. In addition, the probes are used in identifying and characterising storal example should be sufficient to the propes are used in identifying and characterising contained smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human contained to the primined specification, but was obtained to a lettronic format directly from USPTO at
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2000US-00608408
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Best Local Similarity 100.
Matches 20; Conservative
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #9498 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                          100.0%; Score 20; DB 4; Length 600; 100.0%; Pred, No. 9.5;
                                                                                                                                                             Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
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                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 9498; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human placenta.
                                                                                                                                                                                                                                                           1 CGCCGTTCTCCTGGATCCAA 20
                                                                                                                                                                                                                                                                              CGCCGTTCTCCTGGATCCAA 44
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21-SFB-2000; 2000US-023468TP.
25-SEP-2000; 2000US-023468TP.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                          AAI40812 standard; DNA; 600
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                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53
                                                                                                                                                                                                         Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157272-A2
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AAI40812
X8888888888X8
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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart is misconsible by the probes are useful for predicting, diagnosing, srading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                 Probe #7360 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                         Human, gene expression; heart, microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR
CGCCGTTCTCCTGGATCCAA 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCGTTCTCCTGGATCCAA
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                               ABA28894 standard; DNA; 600
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nes 20; Conserv
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Gaps

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100.0%; Score 20; DB 4; Length 600; 100.0%; Pred. No. 9.5; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 20; Conservative

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                              Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                              Human bone marrow expressed single exon probe SEQ ID NO: 9653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 4; Length 600; 100.0%; Pred. No. 9.5; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
31-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK, Chen W,
                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000668
                               (first entry)
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Hes 20; Conservative
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                                                                                                                                                                             WO200157276-A2.
                                                                                                                                              Homo sapiens.
                              06-NOV-2001
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AAK35096;
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Search completed: February 4, 2005, 21:52:42 Job time : 258.033 secs

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Best Loca Matches

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Gaps

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Perfect score:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Janger Intitute Gene Trap Resource - SIGTR.

http://www.sanger.ac.uk/PostGenomics/genetrap/
http://www.sanger.ac.uk/PostGenomics/genetrap/
http://www.sanger.ac.uk/PostGenomics/genetrap/
on Jun 16, 2004 this sequence version replaced gi:48375778.

Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@eanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT0lxr"
/note="Vector: pGT0lxr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ0730 Sanger Institute Gene Trap Library pGT01xr Mus musculus
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BF823588
CLS69565
F08773
BI399503
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CLS69870
CLS69904
BF806802
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BF804861
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/strain="129 OLA"
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                                                                                                                       Class: Gene Trap.
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Best Local Similarity
Matches 20; Conserv
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .; Search time 2384.67 Seconds (without alignments) 305.616 Million cell updates/sec
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AR0269
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AQ0663
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        32822875 seqs, 18219865908 residues
                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                    2005, 20:41:45
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Maximum Match 100%
Listing first 45 summaries
                                                                                nucleic search, using sw model
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CL569805
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                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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gb_htc::
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gb_gs81::
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GSS 16-JUN-2004

CL569565 AP0696 Sa F08773 HSC25B061 n B1399503 MI-P-AY1-AW820481 QV2-ST029 AW244806 BR_END13C

AR1019 Sa AR1031 Sa RC5-RT005

AP0225 Sa AR0485 Sa AR1016 Sa AR1177 Sa PM2-CI011 K-EST0085

CL550034 CL569907 CL569907 CL569868 CL569804 CL569804 CL569804 CL569904 BM818607 BM818607 BF804861 ECC1569871 MF823588 F

AR1032 AR1002

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AQ0669 AQ0670

AQ0654 AS0677

CL570033 A CL569665 A CL569672 A

CL570033 CL569665 CL569672

CL569673

CL569987

Conservative

CGCCGTTCTCCTGGATCCAA

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GSS 16-JUN-2004
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Sanger Intitute Gene Trap Resource - SIGTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On July 16, 2004 this sequence version replaced gi:48375750.

Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.cuk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
                                                                                                                                                  /cell type="Embryonic Stem Cell"
/clone lib="Sanger Institute Gene Trap Library pGT0lxr"
/note="Vector: pGT0lxr"
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/clone lib="Sanger Institute Gene Trap Library pGT0lxr"
/note="Vector: pGT0lxr"
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Larity 100.0%; Pred. No. 47;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Length 119
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Unpublished (2003)
On Jun 16, 2004 this sequence version replaced
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Pred. No.
                                             organism="Mus musculus"
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                                                                                  /strain="129 OLA"
/db_xref="taxon:10090"
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/strain="129 OLA"
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CL569651.2 GI:48774243
                                                                                                                                  sex="Male"
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                                                                                                                                                                                                                                                                                                           20; Conservative
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CL569651/c
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CL569677/c
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A00422 Sanger Institute Gene Trap Library pGT01xr Mus musculus
CDNA, mRNA sequence.
CL569637
                                           GSS 16-JUN-2004
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 107)
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Sanger Intitute Gene Trap Resource - SIGTR.
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Unpublished (2003)
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48375736.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Sequence tag generated by 5, RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
                                                                                                                                                                                                                                                                                                                                               On Jun 16, 2004 this sequence version replaced gi:48375777.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Beali: info.genetrap@sanger.ac.uk
Sequence tag genetrated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
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/note="Vector: pGT0lxr"
                                         CL569678 1007 bp mRNA linear GSS 16-JUN AQ0729 Sanger Institute Gene Trap Library pGT01xr Mus musculus
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Unpublished (2003)
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/mol_type="mRNA"
/strain="129 OLA"
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                                                                               cDNA, mRNA sequence.
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1. .119
/organism="Mus musculus"
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/sex="Male"
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/strain="129 OLA"
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Sanger Intitute Gene Trap Resource - SIGTR.
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Sanger Intitute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
                                                                                                                                                                                                      On Jun 16, 2004 this sequence version replaced gi:48375776.
On Jun 16, 2004 this sequence version replaced gi:48375776.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@eanger.c.uk
Sequence tag generate@eanger.c.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
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Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.
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|clone lib="Sanger Institute Gene Trap Library pGT0lxr"
|note="Vector: pGT0lxr"
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AQ0790 Sanger Institute Gene Trap Library pGT0lxr Mus musculus
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Unpublished (2003)
On Jun 16, 2004 this sequence version renlaced
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/mol_type="mRNA"
/strain="129 OLA"
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strain="129 OLA"
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CL569770 119 bp mRNA linear GSS 16-JUN-2004
AR0256 Sanger Institute Gene Trap Library pGT0lxr Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.
/db_xref="taxon:10090"
/eex="Male"
/cell_type="Embryonic Stem Cell"
/clone lib="sanger Institute Gene Trap Library pGT0lxr"
/note="Vector: pGT0lxr"
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/note="Vector: pGT0lxr"
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AR0269 Sanger Institute Gene Trap Library pGT0lxr Mus musculus
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Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
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us-09-753-169a-7.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 119)

Sanger Intitute Gene Trap Resource - SIGTR.

http://www.sanger.ac.uk/PostGenomics/genetrap/
L Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48376007.

Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
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AR1185 Sanger Institute Gene Trap Library pGT0lxr Mus musculus
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sanger Intitute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
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// clone lib="Sanger Institute Gene Trap Library pGT0lxr"
// note="Vector: pGT0lxr"
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strain="129 OLA"
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CL569911/c
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CL569908/c
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                                                                             http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48375870.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info:genetrappeanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES call lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 119)
Sanger Intitute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 119)
Sanger Intitute Gene Trap Resource - SIGTR.
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Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Bmail: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
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AR0493 Sanger Institute Gene Trap Library pGT01xr Mus musculus
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/strain="129 OLA"
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/strain="129 OLA"
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gi:48376241. SIGTR

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 15)
Sanger Intitute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.
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AV0189 Sanger Institute Gene Trap Library pGT0lxr Mus musculus
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AN0071 Sanger Institute Gene Trap Library pGT0lxr Mus musculus
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Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
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Sanger Intitute Gene Trap Resource - SIGTR.
http://www.sanger.ac.uk/PostGenomics/genetrap/
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced
Contact: Sanger Institute Gene Trap Resource -
Wellcome Trust Sanger Institute
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                              CGCCGTTCTCCTGGATCCAA
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Sanger Intitute Gene Trap Resource - SIGTR.
Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48376010.
On Jun 16, 2004 this sequence version replaced gi:48376010.
Contact: Sanger Institute errap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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/note="Vector: pGT0lxr"
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Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring inscrtion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene Trap.
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Unpublished (2003)
On Jun 16, 2004 this sequence version replaced gi:48376236.
Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
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/mol_type="mRNA"
/strain="129 OLA"
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CL569669 126 bp mRNA linear GSS 16-JUN-2004 AQ0663 Sanger Institute Gene Trap Library pGT0lxr Mus musculus CL569669. CL569669. GI:48774261
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Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from http://www.sanger.ac.uk/PostGenomics/genetrap/
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Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
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/organism="Mus musculus"
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Search completed: February 5, 2005, 08:11:45 Job time : 2385.67 secs

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U34963 Rattus norv
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AR05402 Sequence
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CQ299444 Sequence
CQ293104 Sequence
AX925692 Sequence
AX925694 Sequence
AX925695 Sequence
AX52591 Sequence
XX55912 Sequence
XX55913 Oryctolag
BD084108 Method of
BD102202 Method of
BD102208 Homo sapi
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PR 02-JUL-1998 US 09/109614

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C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
                                                                                                                                                                    BT008248 Synthetic
AF216205 Sus scrof
U72398 Human Bcl-x
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BT008248 Synthetic
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AR380913 Sequence
Z23116 H.sapiens l
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Patent: JP 2002519048-A 8 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/8
PD 02-JUL-2002
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Location/Qualifiers
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PC A61K47/48, A61K48/00, A61P35/00, C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches
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AR380913
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1967.381 Million cell updates/sec
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                                                                                                                                                                                                                                            9053458
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                 4, 2005, 18:10:39
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Listing first 45 summaries
                                                        nucleic search, using sw model
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PD 02-JUL-2002
PF 02-JUL-1999 US 09/109614
PI CY A STEIN
PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
variants that populate a transcriptome
Compugen Inc. (US)
Location/Qualifiers
1. .65
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Patent: JP 2002519048-A 26 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
BN JP 2002519048-A/26
PD 02-JUL-1999 JP 2000557839
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CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
FF Misc binding (1). (4)
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/organism="synthetic construct"
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                                       Oligonucleotide inhibitors of bcl-xL. BD235174
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches
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/ce]l line="WEHI 265.1
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Submitted (26-MAY-1994) Timothy W. Behrens, Medicine, University of
Minnesota, 515 Delaware St. S.E., Minneapolis, MN 55455, USA
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 513)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mMul0100 513 bp mRNA linear ROD :
Mus musculus bcl-x short (bcl-x long) mRNA, complete cds.
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                                         Query Match
100.0%; Score 18; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels
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PE Corporation (NY) (MS)
                                                                                                                                                                                                               Sequence 13703 from Patent W002068579.
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    .512
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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                                                                                                                                                                                                             512 bp
/db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                      31 CTGACTCCAGCTGTATCC 14
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                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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Behrens, T.W.
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CQ727769/c
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/codon_gtart=1
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REFERAINGATGHITPGTAXQSFEQDTFVDLYGNNAAABSRKGGERFNRWFLTGMTVAGV
VLLGSLFSRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MKQSNRELVVDFLSYKLSQKGYSWKQFSDVEENRTEAPEETEPE
RETPSALNGNRSWHLADSPEVNGATCHISSSLDAREVI PWAAVKQALREAGDEFELKYR
RAFEDLTSQLHITPGTAXQSFEQDSFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGV
VLLGSLFSRK"
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He.X.J., Jin,K.L., Graham,S.H. and Simon,R.P.

Direct Submission

Submitted (122-MAR-1999) Neurology, University of Pittsburgh, 3500

Terrace Street, Pittsburgh, PA 15213, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
/cell line="WEHI 265.1 RNA"
/note="alternatively spliced transcript of bcl-x long,
GenBank Accession Number U10101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               10; Length 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF136230 513 bp mRNA linear status norvegicus bcl-x short mRNA, complete cds. AF136230.1 GI:4928687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon start=1
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/protein_id="AAD33683.1"
/db_xref="G1:4928688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10116"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
                                                                                                                             1. .513
/gene="bcl-x long"
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Gaps

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PAT 21-JAN-2004

REFERENCE

JOURNAL REFERENCE AUTHORS

PEATURES

SGO

ORIGIN

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/db_xref="G1:998484"
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ETEPERETEDSAINGNPSWHLADSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDE
FELRYRRAFSDLTSQLTTPGTVYQSFEQDTFVDLYGNNTAPESRKGQERFNRWFLTG
MTVAGVVLLGSLFSRK"
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"Coganism="Homo sapiens"

/mol type="unassigned DNA"

/db_xref="taxon:9606"

/db_x
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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CQ152574
CQ152574.1 GI:41159924
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                                                                                                                                                                                                                                     'note="apoptosis inducer"
                                                                                                                  gene="bcl-xshort"
note="apoptosis inducer"
                           /mol_type="mRNA"
/db_xref="taxon:10118"
1. 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aeomica, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                       gene="bcl-xshort"
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Homo sapiens
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Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserva
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bcl-xshort=apoptosis inducer [rats, ovary, mRNA Partial, 537 nt].
S78284
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RETEGAINGNESWHLADSPAVNGATGHSSSLDAREVI PWAAVKQALREAGDEFELRYR
RAFSDLTSQHIITPGTAYQSFEQDTFVDLYGNNAAAESRKGQERFNRWFLIGMTVAGV
VLLGSLFSRK"
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Tailly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.

Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels

Endocrinology 136 (1), 232-241 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao,G., Chen,J. and Chen,D.
Direct Submission
Submitted (16-JUN-2000) Neurology, University of Pittsburgh, 3500
Terrace Street, Pittsburgh, PA 15261, USA
Location/Qualifiers
                                                                                                                                                                                                    Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Location/Qualifiers
1.537
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            אבעיאבא linear RO
Rattus norvegicus bcl-x short form mRNA, complete cds.
AF279286
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Cao,G., Chen,J. and Chen,D.
BEJ-Xs expression and its role in brain ischemia Unpublished
2 (bases 1 to 513)
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/tissue_type="cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dev_stage="postnatal 1 week"
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/db_xref="G1:8896161"
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TITLE

FEATURES

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1. .555
// Organism="Homo sapiens"
// Arganism="Homo sapiens"
// Mol Lype="unassigned DNA"
// Aref="taxon:9606"
// Aref="taxon:9606"
// Aref="Make TO All17381.9-EXPRESSED IN ADULT LIVER, SIGNAL = 1.5-WISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                                                                                     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENOWE-DEBIUED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130- PB 0004 WO 3<150- US 60/180, 312-215- 04 February 2000 (04.02.00)<150- US 60/207, 456<151- 26 May 2000 (26.05.00)<150- US 60/207, 456<151- 26 May 2000 (26.05.00)<150- US 60/207, 456<151- 03 Gotober 2000 (33.10.00)<150- US 60/234, 687<151- 27 September 2000 (27.09.00)<150- US 60/234, 687<151- 21 September 2000 (21.09.00)<150- US 60/234, 687<151- 21 September 2000 (30.06.00)<170- Molecular Dynamics Sequence Listing Engine Patent: WO 0157273-A 22743 09-AUG-2001;
                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db xref="taxon:9606"
/nore="mAP TO AL1171381.9-EXPRESSED IN FETAL LIVER, SIGNA
= 3.5-SWISSEROT HIT: 007817, EVALUE 1.00e-1.06-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72399.1, EVALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver Patent: WO 0157277-A 21738 09-AUG-2001;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 21738 from Patent WO0157277.
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= 4.7~SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                           Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 22596 09-AUG-2001;
Aeomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0157274-A 17227 09-AUG-2001;
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CQ235904
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/db_xref="taxon:9606"
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VERSION KEYWORDS SOURCE

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Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung

Logene expression in human lung

Aeomica, Inc. (US)

Aeomica, Inc. (
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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το.	Description	Aaz46978 Bcl-X1 mR	Abn55935 Mouse spl	Aba73433 Human foe	Aai53868 Probe #22	Aba38761 Probe #17	Aak48039 Human bon	Aak21876 Human bra	Abs47753 Human liv	Abs21972 Human gen	Ach73889 Human gen	Ach87595 Human gen	Aba60917 Human foe	Aai40812 Probe #94	Aba28894 Probe #73	Aak35096 Human bon	Human	Abs34848 Human liv	Abs09558 Human gen	, Adh52636 Chinese h	Adh52638 Chinese h	Adh52640 Chinese h
SUMMARIES	ID	AAZ46978	ABN55935	ABA73433	AA153868	ABA38761	AAK48039	AAK21876	ABS47753	ABS21972	ACH73889	ACH87595	ABA60917	AA140812	ABA28894	AAK35096	AAK09207	ABS34848	ABS09558	ADH52636	ADH52638	ADH52640
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довда чв в очы	8 100.0 926 12 ADHS2630 8 100.0 926 12 ADO19990 8 100.0 926 12 ADD1331 8 100.0 1236 5 AAS00247 ALIGNMENTS	46978 standard; DNA; 18 BP. 46978; APR-2000 (first entry)	Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Homo sapiens. WO200001393-A2. 13-JAN-2000. 02-JUL-1999; 99WO-US015250.	TUL-1998; 98US-00109614. CO) UNIV COLUMBIA NEW YORK. In CA; ; 2000-137140/12.	ancience of injoint of the regression of vaccular lesions. Useful for reducing bell-attributing one anti-approach procession of vaccular lesions. In vaccular cells to promote the regression of vaccular lesions. In 1; Fig 1; 69pp; English. Invention provides antisense oligonucleotides or their derivatives invention provides antisense oligonucleotides or their derivatives of reduce or eliminate expression of the anti-apoptotic protein bell-are oligonucleotides can be introduced into tumour cells to reduce the oligonucleotides cancer, especially epithelial cancer, e.g. state, lung or bladder cancer, especially epithelial cancer, e.g. state, lung or bladder cancer. Oligonucleotides comprising one or mores with a C-5 propyryl pyrimidine modification may especially be used reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in the treatment. The oligonucleotides can be introduced into vascular is to reduce bcl-xL production to promote the regression of vascular
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptom comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcription unit of the genome, which encodes one or more messenger RNAs ablice variants. The oligonucleotide libraries are useful for detecting mRNAs from a proposition of consistency or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue and encoder a specific genes such as those genes only expressed in specific tissue under a specific genes, and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular developments and mice, which are used in the exemplification of the
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lesions. They can also be included with a carrier (and optionally tetra maso-(4-methylpytidyl)porphine and/or tetra maso-(antilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AZZ46971-983 represent antisense oligos specific for the bcl-X1 mRNA
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                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse spliced transcript detection oligonucleotide SEQ ID NO:28683.
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Best Local Similarity
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splice variant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The
                                                                                                                                                                                                                                                                                                                                                                              Human, foetal liver; gene expression; single exon nucleic acid probe; ss.
present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
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RESULT 4

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular space of cardiovascular disease. Note: The sequence data for this patent of form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
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100.0%; Pred. No. 19;
ive 0; Mismatches
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04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
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Best Local Similarity 100.
Matches 18; Conservative
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                 WO200157274-A2.
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                                                                                                                                                                                                                                                                                                               Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o genome-derived single exon nucleic acid probes useful for analyzing
expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                          Probe #22554 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #17227 for gene expression analysis in human heart cell sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                             Probe; microarray; human; placenta; antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 22554; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
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                                                  AAI53868 standard; DNA; 555 BP.
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2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
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Tes 18; Conservative
                                                                                                                                                                                                                  genetic disorder; ss.
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                                                                                                                                                                                                                                                       Homo sapiens.
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sapiens.
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27-SEP-2000;
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                                                                                                                                                          probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphona, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                         Human, brain expressed exon, gene expression analysis; probe, microarray, Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human brains.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                     present invention provides a number of single exon nucleic acid
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                                                                                                                                  Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                        100.0%; Score 18; DB 4; Length 555; 100.0%; Pred. No. 19;
                                                                                                                                                                                                                     Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe SEQ ID NO: 21867.
                                                                                                                                                                                                                                                            Mismatches
                                                                  Rank DR;
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                                                                                                                 expression in human bone marrow
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                  Chen W,
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468IP.
21-SEP-2000; 2000US-023458IP.
04-OCT-2000; 2000GB-00024263.
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                                                                 Penn SG, Hanzel DK,
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                                                                                    WPI; 2001-488900/53
                                                                                                                                                                                                                                                 Local Similarity
es 18; Conserv
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                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Length 555;
                                                                                                                                                                                                                                                                                                                                      Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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2000US-0207456P.
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Best Local Similarity 100.
Matches 18; Conservative
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ACH73889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes or the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the
                 at
sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                     Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosidarosis, pulmonary hastocytosis, lymphangioleiomyomtosis, Karagener syndrome, pulmonary alveolar proteinosis, fibrocystic pulmonary dysplasia; primary ciliary dyskinesis, pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                              Human genome-derived single exon probe ORF from lung SEQ ID No 21963
                                                                                                                                                                                                                                                                                                                       Human, ds; single exon probe; asthma; lung cancer; COPD; ILD; thronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
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                                                                           Score 18; DB 4; Length 555;
Pred. No. 19;
                                                   Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 measure gene expression in human lung samples.
                                                                                                    Mismatches
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                                                                           Match 100.0%; S
Local Similarity 100.0%; P
es 18; Conservative 0;
                                                                                                                                                     487 CTGACTCCAGCTGTATCC 504
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21-SEP-2000; 2000US-0234687P.
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26-MAY-2000;
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                                                                           Query Match
                                                                                                    Matches
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Targay, Learning 19 predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably calgorithmically predicting at least one exon from genomic sequences of the development and (b) detecting specific hybridisation of detectably can labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the cypobes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene; particularly using human cancer, chronic obstructive pulmonary diseases such as asthma, lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interestitial lung diseases (LDD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary con the probation of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a slingle exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human genome-derived single exon nucleic acid probes useful for huma gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
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identifying exons in a eukaryotic genome, comprising (a)
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Pred. No. 19;
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide according at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification, or their complements or fragaments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that expression (comprising a plurality of single exon nucleic acid molecule expression) comprising a plurality of single exon nucleic acid molecule probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a wector comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid of sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, extended expression data by subscription, and a computer-readable contiguous main which conserve gene expression, a method of providing human gene expression and a computer-readable contended acid including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene capression analysis. The probes may be used as tools for surveying tissues to detect the presence of expression of a single exon microarrays. The admitted measure in detartion and a condition and a contain their specific exon, or in constructing genome-derived single exon microarrays.
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                                        Claim 15; SEQ ID NO 7084; 80pp; English.
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1es 18; Conservative
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The invention comprising any of the 27,400 globe for measuring numan gene sequences in the specification, or their complements or fragments, and sequences in the specification, or their complements or fragments, and cancoling at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality) of single exon microarray for measuring human gene expression, a method of sequence of tited above, where each of the plurality of probes is separately measuring human gene expression, a method of measuring human gene expression, a method of contiguous amino acids of any of the above—mentioned amino acid sequences (optionally with conservative amino acid substitutions), and sequences (optionally with conservative amino acid substitutions), and sequences (optionally with conservative amino acid substitutions), and substance antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene carpression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays.

In addition, the probes are used in identifying and characterising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                         numan genome-derived single exon nucleic acid probes useful for human expression analysis, for identifying or characterizing alternative ring events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid probe for measuring human gene
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
Human; foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
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Pred. No. 19;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
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Best Local Similarity 100.0%;
Matches 18; Conservative 0;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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cardiovascular disease, hypertension, cardiac arrhythmia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 9498; 654pp; English.
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                                                            Rank DR;
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(MOLE-) MOLECULAR DYNAMICS INC
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                                                            Chen W,
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nes 18; Conservative
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us-09-753-169a-8.rng

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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100.0%; Score 18; DB 4; Length 600; 100.0%; Pred. No. 19; Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other; 0; Indels 0; Mismatches Query Match
Best Local Similarity 100.00
These 18; Conservative

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Gaps

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CTGACTCCAGCTGTATCC 523 CTGACTCCAGCTGTATCC 18 506 용 ò

RESULT 15

AAK35096

AAK35096 standard; DNA; 600 BP. AAK35096;

(first entry) 06-NOV-2001 Human bone marrow expressed single exon probe SEQ ID NO: 9653.

Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.

Homo sapiens

WO200157276-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000668

26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0234589P. 04-OCT-2000; 2000GB-00024263. 2000US-0180312P 34-FEB-2000;

(MOLE-) MOLECULAR DYNAMICS INC.

Rank DR

Chen W,

Hanzel DK,

Penn SG,

WPI; 2001-488900/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

Example 4; SEQ ID NO 9653; 658pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention

Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;

Gaps °, Score 18; DB 4; Length 600; Pred. No. 19; Mismatches 0; Indels 100.08; FIL Query Match
Best Local Similarity 100.
Matches 18; Conservative

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523 1 CTGACTCCAGCTGTATCC 18 506 CTGACTCCAGCTGTATCC g à

completed: February 4, 2005, 21:52:43 he : 233.23 secs Job time Search

AMGNINUC: M

170005328 K0244C04-UI-R-Y0-a K-EST0122

BB871778
BB842411
BB842411
BB8523340
BE2533540

BY298104

B0196G01

K-EST0138 AMGNINUC: N

BY096186

OM nucleic

Run on:

Sequence:

Title:

Minimum DB Maximum DB

Database

Result

Searched:

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In (Dates 1 to 279)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other_ESTS: 2822471.3prime
Contact: Robert Straubberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center:

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center:

PHRAP://www.genome.washington.edu

Plate: LLCM9 row: H column: 24

High quality sequence stop: 199.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                              2822471.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822471 5', MRNA sequence.
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/cell line="MGG3"
/lab_nost="DH10B (phage-resistant)"
/clome lib="WHH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAGAG(3). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                   ALIGNMENTS
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2822471"
                                           BB842471
BM855440
BE253353
BY096186
CB775315
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            BB844512
BY055234
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BY281787
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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BY209882
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BY180189
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                                                                           .; Search time 2146.2 Seconds (without alignments)
305.616 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                        32822875 seqs, 18219865908 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      nucleic search, using sw model
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seq length: 200000000
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gb_htc:;;
gb_est4:;
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Musuclula; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Musuraryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Asaes 1 to 287)

Colases 1 to 287)

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yadj.K., Tomaru,Y., Hasegawa,Y., Mogami,A., Kiyosawa,H., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Batelly,K., Blake,J.A., Hill,D.P., Bult,C., Corbani,D.E., Cousins,S., Dalla,E., Dragani,T.A., Chothia,C., Corbani,D.E., Cousins,S., Dalla,E., Dragani,T.A., Garsic,C., Godzik,A., Gough,J., Grimmond,R., Garsic,C., Garsicha,S., Hirokawa,N., Jackson,J.J., Nard,D.J., Kanagani,T.A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurokhin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltas,L., Marchionni,L., MoKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Pesole,G., Pertardo,R., Wollender,C., Semple,C.A., Setou,M., Shimada,K., Schneider,C., Rend,J., Ranachandran,S., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sandia,M., Yang,L., Yang,L., Yang,L., Wang,Y., Wangye,B.R., Tarakana,P., Taylor,M.S., Tarasada,P., Yang,L., Yang,L., Wang,L., Wan
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24/ DP mRNA linear EST 10-DEC-200 CDNA clone F930048G15 5', mRNA sequence.
the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Anzawa, K., Akimura, T., Arakawa, T., Carnindi, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishi, Y., Itoh, M., Kawai, J., Komno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazune, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
                                                                                                                                                                                                                                                                          Gaps
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0
                                                                                                                                                                                           Length 279;
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Mus musculus
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TITLE

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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a norredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequence din Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 313)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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/clone_lib="RIKEN full-length enriched, adult inner ear"
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National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgun.grc.nia.nih.gov
Plate: B0840 row: B column: 09
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100.0%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |db_xref="taxon:10090"
|clone="F930048G15"
|tissue_type="inner ear"
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High quality sequence stop: 313
POLYA-No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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us-09-753-169a-8.rst

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Fax: 847-50-2016

Banail: genome-res@spc.riken.jp, UKL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakaume,N., Sasaki,D., Sato,K., Shibata,,
Ohno,M., Sakai,K., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of FN11-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
COMPUTER-based methods for the mouse full-length cDNA
encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayateu, N., Hirozane-Rishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sakot, K., Sakazume, N., Sakot, K., Hara, A., Hashizume, W., Imotani, K., Kawai, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Ishi, M., Xagawa, T., Mayazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/tissue type="activated spleen"
/clone_Tib="RIKEN full-length enriched, activated spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 320;
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100.0%; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/strain="NOD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGACTCCAGCTGTATCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
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Best Local Similarity
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DEFINITION
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                                                                                                                                                                                                                                                           Mammalia; kucheria; kodencia; sciurognachi; muilude; muilide; muilide; muilide; la (bases 1 to 320)
Okazaki,Y., Puruno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kijosawa,H., Yagi,K., Tomaru,Y., Hasqawa,T., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Baisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustinoich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Nalais,L., Namata,K., Okido,T., Pavan,W.J., Pertead,G., Pesole,G., Petrovsky,N., Pallai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Red,J.C., Reed,J.C., Reed,J.C., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sullana,R., Takenaka,Y., Taylor,M.S., Taasdale,R., Tamita,M., Varagisawa,M., Yang,I., Walls,C., Wilming,L.G., Wynshaw-Boris,A. Yanagisawa,M., Yang,I.,
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cDNA clone F830217H02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                              clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                               /clone="NIA:B0840B09 IMAGE:30471284"
/dev stage="Newborn Kidney"
/lab host="DH10B"
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100.0%; Pred. No. 1.7e+02;
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   /mol_type="mRNA"
/strain="C57BL/6J"
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Best Local Similarity 100.
Matches 18; Conservative
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/clone="UI-M-BH2.1-aps-a-07-0-UI" |
/dev stage="27-32 days" |
/dev stage="27-32 days" |
/dev stage="27-32 days" |
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/clone lib="Will-BMAP_M S3.1" |
/note="Vector: p7713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH-BMAP_M S3.1. |
/note="Vector: p7713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH-BMAP_M S3.1. |
/note="Vector: p7713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NIH-BMAP M S1.1 |
/note="Vector: p7713D-Pac (Pharmacia) with a mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTS had already been generated. The following serially subtracted library (NIH BMAP_M S2, NIH BMAP_M S3.1, NIH BMAP_M S3.1) was constructed as follows: PCRamplified cDNA inserts from NIH BMAP_M S2 clones from which 3 ESTS had been derived was used as driver in a hybridization with the NIH BMAP_M S2 sibrary in the form of single-stranded circles. The Femaining simple carranded circles of simple carranded circles. The Femaining simple carranded circles of simple carranded circles. The Femaining simple carranded circles of simple carranded c
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 320, G. and Soares, M.B.
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made determined by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH BMAP M S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single-stranded circles (subtracted library) was puriby hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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TAG LIB=NIH BMAP M S3.1
TAG SEQ=TCGA"
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/strain="C57BL/6J"
                                                                                                                                         Mus musculus (house mouse)
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                                                                GI:6100730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                         Mus musculus
                                                                AW125200.1
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source

FEATURES

Length 322;

100.0%; Score 18; DB 2;

Query Match

ORIGIN

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Ackaraki, Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaguj, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yaguj, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Paldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalo, S., Brusic, V., Chothia, C., Corbani, L. B., Coustins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibodi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kavoji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lee, Y., Lehnard, B., Lyons, P. B., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Schuelder, C., Semple, C.A., Setou, M., Shimada, K., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Schneider, C., Semple, C.A., Setou, M., Yang, I., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wallain, Y., Itoh, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Sato, K., Shiraki, T., Waki, K., Enders, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNa
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 325)
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imceni,K., Ishli,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
                                                         Gaps
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BY191347 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus CDNA clone F630320F03 5', mRNA
Pred. No. 1.8e+02;
Mismatches 0;
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BY191347.1 GI:26366310
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Matches 18;
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1 (Joages I. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosava, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.B., Cousine, S., Dalaa, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godaik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurcchkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Martais, L., Marchionni, L., McKenzie, L., Mithi, Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasai, T., Red, J.C., Reed, J.C., Reed, J.C., Red, J., Ringy, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Sectou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Wang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninoi, P., Wang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninoi, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computeribes methods for the mouse full-length cDNA nord-dundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Res. 11 (2), 281-289 (2001) cDNA library was Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Fissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addabtookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 327)
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'clone="F630320F03"
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/strain="NOD"
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Email: genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozanne,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
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Computer-based methods for the mouse full-length construction of a
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convalization was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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BY219527
                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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/clone_lib="RIKEN full-length enriched, B6-derived CD11
+ve dendritic cells"
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                              Nature 420, 563-573 (2002)
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Length 336; Indels

ORGANISM

KEYWORDS SOURCE

VERSION

AUTHORS

REFERENCE

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zr28c08.rl Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664718 5' similar to TR:G998484 G998484 BCL-XSHORT-APOPTOSIS INDUCER; mRNA sequence.
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/dev_stage="Ntera-2 neuroepithelial cells"
/lab host-="SOLR (kanamycin resistent)"
/clone_lib="StratentNT neuronal precursor 937230"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
BcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Uninduced, exponentially growing neuroepithelial
cells (Ntera-2/Cl.DI). Average insert size: 1.0 kb;
                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases, 1 to 339)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hukkins,M., Hulkman,M., Kucaba,T., Lacy,M., Le,N., Le,N., Bonatis,E., Moore,B., Moore,B., Soares,M.B., Parange,C., Prange,C., Riffin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1800
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seg primer: -28ml3 revu ET from Amersham
High quality sequence stop: 175.
Location/Qualifiers
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:664718"
/tissue_type="neuroepithelial cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                  organism="Mus musculus"
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/db_xref="GDB:5426748"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="F830115M14"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                               /mol_type="mRNA"
/strain="NOD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 CTGACTCCAGCTGTATCC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGACTCCAGCTGTATCC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                     Mikaido, I., Osatoria i Sciurognatni; Muridae; Murinae; Mus. 1 (Dases I to 336)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, M., Saito, R., Suzuki, H., Yangai, R., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Paldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schrimi, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Pacdt, D., Brusic, V., Ratelli, R., Fracer, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.A., Garibodi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Karochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Magashima, T., Namtas, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Raachandran, S., Ravasi, T., Reed, J.C., Red, D.J., Reid, J., Ring, B. E., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, N.S., Taskanaba, Y., Watanabe, Y., Watanabe, Y., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wang, L., Yang, L., Hara, A., Hashizum, W., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analyasa, C., Bhinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, D., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length connerty and the state of the connerty of the 
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Inchani,K., Ishli,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), i617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA methods for the mouse full-length construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Spiloration in Riken Division of Experimental Animal Research in Riken contributed to
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics vealloome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre Area Hospital Cambridge) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                         Mus musculus (house mouse)
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Fax: 81-45-503-9216
                                                                                                                                       Mus musculus
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MEDLINE PUBMED

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JOURNAL

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Musmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 341)

Sukarycota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 341)

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kuyadawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Mateuda, H., Batsel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousines, S., Dalla, E., Dragani, T.A., Glasi, C., Godzik, A., Gough, J., Girmmond, S., Gustincich, S., Hirokawa, N., Jackson, J.J., Mardi, E.D., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., MoKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petardok, D., Marchionni, L., Mokenzie, L., Miki, H., Nagashima, T., Rawasi, T., Pakenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Schneider, C., Reed, D.J., Reading, B.Z., Ringwald, M., Sullana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verado, R., Wagner, L., Wahlested, C., Wangy, Y., Watanabe, Y., Mayor, L., Wallana, R., Takenaka, Y., Taylor, M.S., Yanagisawa, M., Yang, I., Wayatsu, N., Sato, K., Shirak, T., Wan, Y., Yangisawa, M., Yang, I., Wayatsu, J., Watanabe, S., Hara, A., Hashiaume, M., Takawa, T., Fukuda, S., Hara, A., Hashiaume, M., Takawa, T., Luch, M., Kagawa, I., Waki, K., Kawai, J., Alakawa, K., Shinagawa, A., Yasuishi, A., Satok, M., Waterston, R., London, M., Waterston, R., Lang, R., Satok, J., Satok, M., Satok, M., Satok, M., Satok, M., Satok, M., Satok, S., Hara, A., Hashiaume, W., Tawcation, R., Satok, S., Hara, A., Hashiaume, M., Satok, S., Hara
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-922
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
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Figure Compenses Fax: 81-45-503-9216
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                                                                                                                                                                                                                           Length 339;
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Pred. No. 1.8e+02;
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1 Similarity 100.0%; P1
18; Conservative 0;
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SOURCE

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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Construction of Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics mellower Trust Centre for Molecular Mechanisms in Disease Wellcome
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 344)
S Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Kouno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toyawa,A., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone="F630021E08"
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/strain="NOD"
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Intestinal mucosa,
dev stage=adult, sex=male), (tissue type=accessory
axillary lymph node, dev_stage=adult, sex=male),
(tissue_type=galul bladder,
dev_stage=adult, sex=male), (tissue_type=gall bladder,
dev_stage=all days embryo), (tissue_type=spinal cord,
dev_stage=11 days embryo), (tissue_type=brain,
dev_stage=13 days embryo), (tissue_type=brain,
dev_stage=13 days embryo), (tissue_type=brain,
dev_stage=13 days embryo), (tissue_type=prain,
dev_stage=10 days embryo), (tissue_type=brain,
dev_stage=10 days embryo), (tissue_type=cortex,
dev_stage=10 days embryo), (tissue_type=cortex),
dev_stage=10 day neonate), (tissue_type=cortebalum,
dev_stage=1 month neonate, sex=male), (tissue_type=medulla
oblongata, dev_stage=16 days neonate, sex=male),
(tissue_type=cortebellum, dev_stage=21 days neonate, sex=male)"
(tissue_type=cortebellum, dev_stage=21 days neonate, sex=male)"
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                                                                                                                                                                                                                                                                                                                                                            sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashi, X.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                        Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci.P., Shibata.Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Maramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fuliwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="RIKEN full-length enriched, pooled tissues,
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/mol_type="mRNA"
/strain="C57BL/6"
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Nammalis, Ritheria, Rodentis, Sciurognathi, Muridae; Musine, Mammalis, Ritheria, Rodentis, Sciurognathi, Muridae; Musine, Morasali, T., Purton, M., Senakae, T., Adachi, J., Buord, H., Rondo, S., Romano, T., Purton, M., Senakae, T., Adachi, J., Buord, H., Rodo, S., Romano, T., Burden, J., Rangae, H., Rogan, P., Schonbech, T., Radicali, M., Blake, J., Brade, D., Brait, C., Hume, D. A., Ouskenbanh, J., Schrämi, L.M., Endan, J., Brade, D., Bruit, C., Hume, D. A., Ouskenbanh, J., Schrämi, L.M., Endan, J., Brade, D., Bruit, C., Hume, D. A., Ouskenbanh, J., Schrämi, L.M., Endan, J. Brade, D., Bruit, C., Hume, D. A., Ouskenbanh, J., Schrämi, L.M., Endan, B., Brade, B., Brade, D., Kanai, A., Rachon, J., Brade, D., Bruit, D. P., Ball, C., Gurine, M., Malan, B., Man, M., Malan, J., Marchis, D., Kanai, A., Marchis, D., Kanai, A., Marchis, M., Marchis, D., Kanai, A., Marchis, M., Marchis, M., Marchis, D., Kanai, M., Marchis, M., Sadd, D., Sadd, M., Marchis, M., Schallin, A., Schnader, C., Sector, M., Shimada, K., Sadd, D., Sadd, M., Sadd, M.,
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ORIGIN

SOURCE

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source
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ORGANISM
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KEYWORDS
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Okazaki, Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Eletcher, C. F., Forrest, A., Frazer, K.S., Gaasterland, T., Chothia, C., Corbani, L. E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godaik, A., Gough, J., Grimmond, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lee, Y., Lennard, B., Lyons, P.A., Magoshima, T., Narchionni, L., Marchionni, L., McKenie, L., Mith, H., Nagashima, T., Navasi, T., Reed, J. C., Reed, D.J., Ramachadran, S., Sandelin, A., Schneider, C., Reed, D.J., Ranglaawa, M., Shimada, K., Sanger, L., Wahlested, C., Wang, Y., Warnagisawa, M., Yang, I., Yang, L., Wanger, L., Wanseted, C., Wang, Y., Warnach, Y., Wanger, L., Wahlested, C., Wang, Y., Warnach, Y., Wanger, L., Wahlested, C., Wang, Y., Warnach, Y., Wanger, L., Wahlested, C., Wang, Y., Warnach, Y., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sato, K., Shirak, Y., Wang, Y., Arakawa, T., Pukuda, S., Hara, A., Hashizume, M., Tmotani, K., Ishik, Y., Roper, M., Shibata, K., Shinay, A., Shihata, Y., Wang, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY058101
BY058101 RIKEN full-length enriched, TIB-55 BB88 Mus musculus cDNA
/cell line="RCB-0558 LLC"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
cDNA"
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-45-503-9216
Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishli,Y., Itch,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                     Length 348;
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                  100.0%; Score 18; DB 5; L 100.0%; Pred. No. 1.8e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone 1730095E04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                  288 CTGACTCCAGCTGTATCC 271
                                                                                                                                                                                                                                                                                                                                           1 CTGACTCCAGCTGTATCC 18
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                                                                                                                                                                                                                                                                          Conservative
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Matches 18; Conserv
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KEYWORDS
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to sequence integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikado,I., Osatco,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Belsel,K.W., Blake,J.A., Brudi,D., Brusic,V.,
Chothia,C., Corbani,L.B., Cousins,S., Dalla,B., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Kawaii,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Mixi,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Phllai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Tasasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_line="TIB-55 BB88"
/clone_lib="RIKEN full-length enriched, TIB-55 BB88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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/clone="1730095E04"
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/strain="BALB/c"
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Best Local Similarity 100.0
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MEDLINE PUBMED

COMMENT

JOURNAL

TITLE

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Musmalia, Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Muscaulus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Rogers, J., Shiray, E., Hara, A., Hashizume, W., Saski, C.,

Rogers, J., Sasto, K., Yang, Sasto, 
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The Institute of Physical and Chemical Research (RIKEN)
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Email: gnome-reseggs.riken.jp, URL:http://genome.gsc.riken.jp/
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Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs.Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Genome
Encyclopedia Project of Genome Exploration Research Genome
Encyclopedia Project of Genome Exploration Research for prisures
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missure mouse full-library and Genome Science Laboratory in RIKEN
pivision of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                      fus musculus (house mouse)
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                                      SOURCE
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Alzawa, K., Akimura, T., Arawawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, M., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse CDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length CDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Azawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Shiakawa,T., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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355 bp mRNA linear EST 10-1
BY180189 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus CDNA clone F630038P12 5', mRNA
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DEFINITION RESULT 15 BY180189/c

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VERSION KEYWORDS

Matches

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Location/Qualifiers

1. 355

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AR3116 G. Sequence
AR380913 Sequence
AX12772 Sequence
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AX127818 Sequence
AR14952 Sequence
AR149311 Sequence
AR14311 Sequence
AR14312 Sequence
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Patent: JP 2002519048-A 9 02-JUL-2002;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Patent: JP 2002519048-A 28 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/28
PD 02-JUL-1999 JP 2000557839
PF 02-JUL-1999 US 09/109614
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ANTISENSE OLIGONUCLEOTIDE

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FF Misc binding (1). (1)

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Patent: WO 02068579-A 13703 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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                                                               Oligonucleotide inhibitors of bcl-xL. BD235176
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(11)..(12)
(15)..(18).
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/organism="synthetic cc
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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misc_binding (5)...(7)
misc_binding (9)...(10
misc_binding (11)...(1)
misc_binding (15)...(1)
Location/Qualifiers
                                                                                                                                          BD235176.1 GI:33044946
JP 2002519048-A/28.
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1 (bases 1 to 18)
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Homo sapiens
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synthetic construct
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Matches 18; Conservative
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Patent: JP 2002519048-A 27 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/27
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1999 US 09/109614
PI CY A STEIN
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0; Mismatches 0; Indels
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/mol_type="genomic DNA"
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                                                                                                      18 bp DN.
Oligonucleotide inhibitors of bcl-xL.
BD235175
BD235175.1 GI:33044945
JP 2002519048-A/27,
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                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
Patent: WO 0157276-A 22596 09-AUG-2001;
Aeomica, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                          Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
Patent: WO 0157272-A 22554 09-AUG-2001,
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Sequence 22554 from Patent WO0157272.
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Pred. No. 80;
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                               Mismatches
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/db_xref="taxon:9606"
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Location/Qualifiers
1. .555
/organism="Homo sapiens"
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Pred. No.
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/organism="Homo sapiens"
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Location/Qualifiers
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CQ152574.1 GI:41159924
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/db_xref="taxon:9606"
/note="Map TO AL117381.9~EXPRESSED IN BONE MARROW, SIGNAL
= 4.7~SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
0.00e+00"
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HUMMAN GENOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> Of February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> OS 0000 (03.08.00)<150> US 60/203,456<151> OS 0000 (03.08.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000
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1.4-SWISSPROT HIT: Q07817, EVALUE 1.00e-106-EST HUMAN 1
BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0157274-A 17227 09-AUG-2001;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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CQ235904.
CQ235904.1 GI:41219182
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Sequence 17227 from Patent WO0157274.
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Llarity 100.0%; Pred. No. 80;
Conservative 0; Mismatches
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larity 100.0%; Pred. No. 80;
Conservative 0; Mismatches
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Location/Qualifiers
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FEATURES

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/organism="Homo sapiens"
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                                                                           Aeomica, Inc. (US)
Location/Qualifiers
1. :555
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid analysis of gene expression in human lung patent: WO 0186003-A 21963 15-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid analysis of gene expression in human brain Aecmica, NO 0157275-A 21867 09-AUG-2001; Aecmica, Inc. (US)
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red. No. 80;
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100.0%; Pred. No. 80;
iive 0; Mismatches
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larity 100.0%; Pred. No. 6
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CQ100639.1 GI:41069665
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CQ347773.1 GI:41296844
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Matches 18; Conserv
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Matches 18; Conserv
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CQ347773
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                                                                                              1. :555.

| Organism="Homo sapiens"

| Mol Lype="unassigned DNA"

| Ab Aref="taxon:5666"

| Note="MAP TO AL117381.9-EXPRESSED IN ADULT LIVER, SIGNAL

= 1.7-SWISSPROT HIT: Q0'817, EVALUE 1.00e-106-EST HUMAN

HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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= 3.5~SWISSPROT HIT: Q07817, EVALUE 1.00e-106~EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00~NT HIT: U72399.1, EVALUE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine Patent: WO 0157273-A 22743 09-AUG-2001;
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Human genome-derived single exon mucleic acid probes useful
analysis of gene expression in human fetal liver
Patent: WO 0157277-A 21738 09-AUG-2001;
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Location/Qualifiers
                                                        Aeomica, Inc. (US)
Location/Qualifiers
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CQ310858.1 GI:41271435
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Homo sapiens
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DEFINITION

RESULT 9 CQ273477 LOCUS

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="texcon:9606"
/noTe="MAP TO AL117381.9~EXPRESSED IN BONE MARROW, SIGNAL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9-EXPRESSED IN PLACENTA, SIGNAL 0.99"
              Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 9498 09-AUG-2001;
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Human genome-derived single exon nucleic acid probes useful for
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 9653 09-AUG-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Sequence 9653 from Patent W00157276.
CQ139631.1 GI:41097003
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Sequence 7360 from Patent WO0157274.
CQ175964
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CQ139631
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CQ175964
                                                             JOURNAL
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                                                                                           FEATURES
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/nb_xref="taxon:9606"
/nb="MAP TO AL117381.9~EXPRESSED IN ADULT LIVER, SIGNAL
= 1.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER-130- PB 0004 WO 3<br/>
3<br/>
150-00 US 60/1806,312<br/>
150/207,456<br/>
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                            /mol type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Length 600
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analysis of gene expression in human heart
Patent: WO 0157274-A 7360 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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tive 0; Mismatches
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Sequence 9838 from Patent WO0157273.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February Run on:

4, 2005, 15:50:53; Search time 232.23 Seconds (without alignments) 406.880 Million cell updates/sec

US-09-753-169A-9 18 Perfect score: Title:

1 ggtctccatctccgattc 18 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4134886 segs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04: Database :

geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2003cs:* geneseqn2002as:* geneseqn2003as:* geneseqn2001bs:* geneseqn2002bs:* geneseqn2004s:* geneseqn2003bs: geneseqn2003ds; geneseqn1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaz46979 Bcl-Xl mR	Aba73433 Human foe	Aai53868 Probe #22	Aba38761 Probe #17	Aak48039 Human bon	Aak21876 Human bra	Abs47753 Human liv	Abs21972 Human gen	Ach73889 Human gen	Ach87595 Human gen	Aba60917 Human foe	Aai40812 Probe #94	Aba28894 Probe #73	Aak35096 Human bon	Aak09207 Human bra	Abs34848 Human liv	Abs09558 Human gen	Aah48169 Mutant bc	Aah43464 cDNA clon	Adm45994 Human apo	Aaq81699 Human thy
SUMMAKIES	f	1D	AAZ46979	ABA73433	AAI53868	ABA38761	AAK48039	AAK21876	ABS47753	ABS21972	ACH73889	ACH87595	ABA60917	AA140812	ABA28894	AAK35096	AAK09207	ABS34848	ABS09558	AAH48169	AAH43464	ADM45994	AAQ81699
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Abz83507 Toxicolog Adi32132 Human cDN Adg65218 Human Bcl Aaf30926 Human Bcl Adg65209 Human Bcl	Aaq81698 Human thy Aat40079 BC1-KL ge Aaz93614 BC1-x gen Aas15189 Human bc1	Aac90810 Human BC1 Abk84766 Human CDN Abt16641 Human bc1 Add86779 Human bc1 Aad64187 Human bc1 Aad64187 Human bc1	Adi32104 Human cDN Adh52630 Human ant Ado19990 Human PRO Adp13351 Renal cel Aas00247 Bcl-Xl-DT	Aas00250 LFn-Bcl-X Adg89403 Cancer de Adn04260 Antipsori Ado19866 Human PRO Aax33182 Base sequ
ABZ83507 ADI32132 ADG5218 AAF30926 ADG65209	AAQ81698 AAT40079 AAZ93614 AAS15189	AAC90810 ABK84766 ABT16641 ADD56779 AAD64187	ADI32104 ADH52630 ADO19990 ADP13351 AAS00247	AAS00250 ADG89403 ADN04260 ADO19866 AAX33182
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ALIGNMENTS

Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Bcl-X1 mRNA specific antisense oligo I. AAZ46979 standard; DNA; 18 BP. 14-APR-2000 (first entry) Homo sapiens. AAZ46979; RESULT 1

WO200001393-A2.

13-JAN-2000.

99WO-US015250. 02-JUL-1999; 98US-00109614. 02-JUL-1998; (UYCO) UNIV COLUMBIA NEW YORK.

Stein CA;

WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

which reduce or eliminate expression of the anti-apoptotic protein bcl-k. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-z family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular The invention provides antisense oligonucleotides or their derivatives

Probe #22554 used to measure gene expression in human placenta sample.

(first entry)

17-OCT-2001

AAI53868;

AAI53868 standard; DNA; 555

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RESULT 3
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lesions. They can also be included with a carrier (and optionally tetra meso- (4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-Xi mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                            100.0%; Score 18; DB 3; Length 18; 100.0%; Pred. No. 30;
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                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                Human foetal liver single exon nucleic acid probe #21738.
                                                                              Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-0234687P
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Best Local Similarity 100.
Matches 18; Conservative
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les 18; Conserv
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #17227 for gene expression analysis in human heart cell sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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                                                                             microarray; human; placenta; antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 22554; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                   DR;
                                                                                                                                                                                                                                                                                                                                                                   Rank
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                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                          26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                             04-OCT-2000; 2000GB-00024263
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488897/53
                                                                                            genetic disorder;
                                                                                                                                                WO200157272-A2
                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                               04-FEB-2000;
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                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA38761;
                                                                              Probe;
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; DB 100.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                     Rank DR
                                                                                                                                                                                                                                              gene expression in human bone marrow.
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                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
30-JUN-2000; 2000US-0060840B.
03-MG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235359P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408.
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                        WPI; 2001-488900/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in a sample derived from human heatr. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 18; DB 4; Length 555; 100.0%; Pred. No. 39;
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                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                 2000US-0207456P.
2000US-00608408.
2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
                                                                                                             30-JAN-2001; 2001WO-US000666
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                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488899/53
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                                    WO200157274-A2
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 Homo sapiens.
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                                                                         09-AUG-2001
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                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single exon nucleic acid probes useful for analyzing
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                             Example 4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 18; DB 4; Length 555; 100.0%; Pred. No. 39; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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2000US-00608408.
2000US-00632366.
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                         invention
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ABS4775
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liver single exon nucleic acid probes of the invention. Note: The agequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; daucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiccytosis; lymphangioleiomyomicosis; Karagener syndrome; pulmonary diveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon probe ORF from lung SEQ ID No 21963.
                                                                                                                                                         Gaps
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                                                                                                                       Length 555;
                                                                                      Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                         0; Indels
                                                                                                                         4,
                                                                                                                       DВ
39;
                                                                                                                                                        0; Mismatches
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                                                                                                                       100.0%; Score 18; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                            1 GGTCTCCATCTCCGATTC 18
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                424 GGTCTCCATCTCCGATTC
                                                                                                                                                                                                                                                                                                                 ABS21972 standard; DNA; 555
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                  Query Match
Best Local Similarity 100.
Matches 18; Conservative
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                 RESULT 8
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array; identifying exons in a entaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detectain specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the comprising frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (LLD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Ptck disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frame of the id not form part of conic format directly
   measuring the label detectably bound to each probe of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part the printed specification, but was obtained in electronic format dire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the printed specification, but was obtained in electrofrom WIPO at ftp.wipo.int/pub/published_pct_sequences
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100.0%; Score 18; DB 6; Length 555; 100.0%; Pred. No. 39; 0; Indels ive. 0; Mismatches 0; Indels Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other; 1 GGTCTCCATCTCCGATTC 18 Query Match Best Local Similarity 100.0 Matches 18; Conservative g ò

Gaps

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441 424 GGTCTCCATCTCCGATTC

ACH73889 standard; DNA; 559 BP (first entry) 29-JUL-2004 ACH73889; RESULT 9 ACH73889

Human genome derived single exon probe #7084.

Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration. Human;

Homo sapiens

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative
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The invention relates to a nucleic acid probe for measuring numan gene expression, comprising any of the 37,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and sequences in the specification, or their complements or fragments, and concoling at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or itssues. Also included are a spatially.

C addressable set of single exon nucleic acid probes for measuring human cells or tissues. Also included are a spatially.

C and addressable set of single exon nucleic acid probes is separately and addressably isolatable or amplifiable from the plurality), a single configuration of succession, a method of measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8

C measuring human gene expression, a vector comprising at least 8

C measuring human gene expression, a method of providing contiguous amino acids of any of the above mentioned amino acid and of a licensing single exon probes or microarrays to sequences (optionally with conservative amino acid substitutions), an estomer desiring to measure gene expression of a single exon probe contain desire and any ene expression act aby subscription, and a computer-readable caused methods of selling and/or licensing single exon probes contain their corrage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe conted and probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in raining the synthesis of mucleic acids. ö smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at invention relates to a nucleic acid probe for measuring human gene Gaps events, for assessing genomic alterations or as tools for ; 0 100.0%; Score 18; DB 12; Length 559; 100.0%; Pred. No. 39; Sequence 559 BP; 138 A; 169 C; 107 G; 145 T; 0 U; 0 Other; Indels segdata.uspto.gov/sequence.html?DocID=20030194704 Mismatches Claim 15; SEQ ID NO 7084; 80pp; English. ö Conservative Local Similarity es 18; Conserv splicing Query Match Matches à

1 GGTCTCCATCTCCGATTC 18

ACH87595 standard; DNA; 564 BP 19 GGTCTCCATCTCCGATTC 36 (first entry) 29-JUL-2004 ACH87595; RESULT 10 ACH87595 셤

Human, probe, 88, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration. Human genome derived single exon probe #20790.

Homo sapiens

US2003194704-A1

16-OCT-2003.

03-APR-2002; 2002US-00029386

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04-FEB-2000; 2000US-0180312P
26-MAY-2000; 2000US-0207456P
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                                               Homo sapiens.
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                                                                                                                                                                                                                                                   The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and sequences in the specification, or their complements or fragments, and sequences in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially.

Comprising a plurality of single exon nucleic acid probes for measuring human cells exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a wetton comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid contiguous amino acids of any of the above- mentioned amino acid substitutions), an operation of selling and/or licenship single exon probes or microarrays to sequences (optionally with conservative amino acid substitutions), and sequences (optionally with conservative amino acid substitutions), and sequences (optionally with conservative amino acid substitutions), and sequence desiring to measure gene expression, a method of providing to measure gene expression of a single exon probe or microarrays to a customer desiring to measure gene expression of a single exon probe or methods of selling and/or licenship single exon probe or microarrays to a customer desiring to measure gene expression of a single exon probe or the probes may be used as tools for surveying tisques and apparatus and characterising gross are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising gross alternations in the genomic locus that includes their events of microarray or in expressing the 
                                                                                                                                                 New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
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                                                                                                                                                                                                                              Claim 1; SEQ ID NO 20790; 80pp; English
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                                                                                        Penn SG, Rank DR, Hanzel DK;
03-APR-2002; 2002US-00029386
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                         (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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Best Local Similarity
                                                                                                                                                                                                  surveying tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
Human; foetal liver; gene expression; single exon nucleic acid probe; ss
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21-SEP-2000; 2000US-0234687P.
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                          Gaps
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    Claim 1; SEQ ID NO 7360; 530pp; English.
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                                                                                                                                                                                                                                                                                                      1 GGTCTCCATCTCCGATTC 18
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2000US-0236359P.
2000GB-00024263.
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Best Local Similarity
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                             4; Length 600;
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                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                        Claim 25; SEQ ID NO 9498; 654pp; English.
                                                                                                                    Chen W, Rank DR;
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                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
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              03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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Matches 18, Conservative
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            03-AUG-2000;
21-SEP-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                  Gaps
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ch 100.0%; Score 18; DB 4; Length 600; I Similarity 100.0%; Pred. No. 39; 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                       Human brain expressed single exon probe SEQ ID NO: 9198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                443 GGTCTCCATCTCCGATTC 460
                                                                                                                                                                          AAK09207 standard; DNA; 600 BP.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
                                                               1 GGTCTCCATCTCCGATTC 18
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                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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Search completed: February 4, 2005, 21:52:43 Job time : 232.23 secs

443 GGTCTCCATCTCCGATTC 460

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603031642 EST544881 ba09f05.y UI-HF-EL0 603256193

56049223J

Minimum DB Maximum DB

Database

Result

Searched:

601058641

603185360 602766132

EST583858

170005326

OM nucleic

Run on:

Sequence:

Perfect

Title:

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243 bp mRNA linear EST 22-JAN-2002 tomato breaker fruit Lycopersicon esculentum cDNA clone 5' end, mRNA sequence.
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/note="Vector: pBluescriptSKmCUadapt, Site 1: EcoR1;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
Iyoopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 243)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A.,
Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
                CN422268
BECR3664
BECR33307
CF132307
CF132307
CF132364
BI49889
BI502264
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BI507063
BNG10652
BNG1
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/organism="Lycopersicon esculentum"
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Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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/dev_stage="breaker"
/lab_host="SOLR"
                                  BE783664
BE206897
                                                                 CF132307
CF131456
CN422264
BI489889
BI924992
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/clone="clEG50N22"
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CD636467
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Location/Qualifiers
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/cultivar="TA496"
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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ORIGIN
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EST340806
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305.616 Million cell updates/sec
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                                                                                                                  20:41:45 ; Search time 2146.2 Seconds
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          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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seq length: 200000000
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Tracheophyta;

GSS 06-DEC-2000

RESULT 2 AW247015/c

q

Matches

DEFINITION

ACCESSION VERSION

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Aurora Biosciences Corp.

11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8884046436
Fax: 8584046413
Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin reaistance followed by a splice donor to trap downstream exons. 3' RACB from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DHS-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Genetrap T47D Human Breast Carcinoma Library" /note="Organ: Breast; Vector: pAmp-1; 3' RACE of total RNA from genetrap pole; shotgun clone in pAmp-1 and used to transform D45-alpha competent bacteria."
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                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 344)
Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M.,
Exon-trap tags from a T47D GenomeScreen(TM) Library
Unpublished (2000)
AZ576742
AST-2T00919 Genetrap T47D Human Breast Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
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GSS.
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Other ESTS: 282241.3prime
Contact: Robert Strausberg, Ph.D.

Email: cgapbe-remail.inh.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LiNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/Link at:
www-bio.lln.gov/bbrp/image/aimage.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu
Plate: LiCM9 row: H column: 24
High quality sequence stop: 199.
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/tissue type="smail cell carcinoma"
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/lab host="MHGG"
/clone lib="NHH MGC 7"
/cloned into EcoRI/Xhoi sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                         Gaps
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                           100.0%; Score 18; DB 4; Length 243; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
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FEATURES

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Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
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/mol_type="mRNA"
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/cell_line="SNU-216"
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Plate: 63 row: B column: 03
High quality sequence stop: 421.
Location/Qualifiers
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Best Local Simi
Matches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Stomach"
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/cell_type="Stomach"
/cell_type="Thoating aggregates"
/cell_type="Thoating aggregates"
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/clone phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (BAP). The decapped intact mRNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was adjusted to have about 60nt. The CDNA vector was converted to a DNA strand by Okayama-Berg method. The converted colls E. coli DNA ligase after digestion of competent cells E. coli ToplOff' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
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EST359240 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone CLEF53L24 5', mRNA sequence.
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                                                         Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
7e1: +82-42-860-4470
Fax: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 67 row: G column: 02
High quality sequence stop: 382.
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Generation of ESTs from tomato fruit tissue
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100 Jordan Hall, Clemson, SC 29634, USA
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Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="S21SNU520-67-G02"
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                'mol_type="mRNA"
'db_xref="taxon:9606"
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BM844286 421 bp mRNA linear EST 06-MAR-2002
K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="Toplor" |
/lab host="Toplor" |
/clone lib="$12$NU216" |
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NOTI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
                                                                                                                                                                                                                                                                    /clone lib="tomato fruit mature green, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; cLEF - Fruit were tagged at the lom stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                             /rissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; DB 2; Length 40
100.0%; Pred. No. 2.8e+02;
Artive 0; Mismatches 0; Indels
/organism="Lycopersicon esculentum"
/mol_type="mtNd"
/cultivar=TA496"
/db xref="taxon:4081"
/clone="clEF53L24"
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Contact: CUGI
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Matches 18; Conserv
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AI777656
LOCUS
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AW930419
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="texon:9660"
/clone="INAGE:30569057"
/tissue_type="CNCAP(3)T-225 cell line"
/lab host="blub (TI phage resistant)"
/lab host="blub (TI phage resistant)"
/clone lib="NIH MGC_210"
/note="Organ: Prostate; Vector: pT/T3 Pac; Site_1: EcoR I; Site_2: Not I; The library was constructed according Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a it agarcse gel. First strand cDNA was size fractionated on the oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned
intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of convertent cells E. coli TOplOF, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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MGC_210 Homo sapiens CDNA clone
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coordinated Laboratory for Computational Genomics
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UI-HF-CBO-asn-f-06-0-UI.rl NIH MG'
IMAGE:30569057 5', mRNA sequence.
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Best Local Similarity
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Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (Bases 1 to 453)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratlift."
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/dev stage="mature green (3-5 days pre-ripening)"

/dab_nogte="SOLR"

/dab_nogte="SOLR"

/clone lib="tomato fruit mature green, TANU"

/note="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2:

Xhol; cLEF - Fruit were tagged at the lcm stage and

harvested 3-5 days prior to ripening. Fruit were cut in

half to verify the seeds were indeed 'immature' and the

seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST340792 tomato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF42D3 5', mRNA sequence.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                   Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 453;
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Generation of ESTs from tomato fruit tissue
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                                                                                                                                   Score 18; DB 6; I
Pred. No. 2.8e+02;
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100.0%; Pred. No....
0; Mismatches
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/clone="clEF42D3"
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1, .453
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/cultivar="TA496"
                                                                                                                                                                                                                                                                            138 GGTCTCCATCTCCGATTC 121
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                                                                                                                          Query Match
Best Local Similarity 100.º
Matches 18, Conservative
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      FEATURES
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                                                                               Lycopersion esculentum (Comato).

By Endrance, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Strattophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; asterids; lamids; Solanales; Solanacea; Solanum; Lycopersicon.

[Chases 1 to 455]

D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Lianay,F., Upton,J., Roming,C.M., Craven,M.B., Fujii,C.Y., Glovannoni,J.J. and Martin,G.B.

Generation of ESTs from Pseudomonas susceptible tomato

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="tomato susceptible, Cornell"
/note="Vector: pBlueScript SK(-); Site 1: EcoRl; Site 2:
Xhol; cLES - Tomato Pseudomonas Susceptible EST Library.
Directionally cloned cDNAs inserted into pBlueScript
SK(-) at 5' end with EcoRl and 3' end with Xhol site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Mat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

1 (bases 1 to 474)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
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17000424524125 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
CN422261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"

/mol_type="mRXAX"

/cultiva="R11-13 (Rio Grande x Money Maker)"

/baref="taxon:4081"

/clone="cLES2M16"
                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Length: 474 Std Error: 0.00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="leaf"
/dev_stage="4-week_old"
/lab_host="SOLR"
                                                                 Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AI777656.1 GI:5275613
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Homo sapiens
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Best Local Similarity 100.
Matches 18; Conservative
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Fax: 650 473 7760
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CN422261/c
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AUTHORS
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/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/drisque type="embryonic stem cells, embryoid bodies
/clone lib="GRN EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
HI (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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Gm62c06.xl Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893322 3' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS SECTIVATOR BCL-X. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Roberts Strausberg, Ph.D.
Emall: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1323 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 440.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0;
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organism≃"Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1893322"
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                                                                                                                                                                                                                                                                                                                                                                                                            199 GGTCTCCATCTCCGATTC 182
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BM857244/c DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

TITLE JOURNAL COMMENT

AUTHORS

REFERENCE

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1 (bases 1 to 560)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tisaue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone lib="GRN_EB" from H1, H7 and H9 cells" /note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
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  EST 16-MAY-2004
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 542)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

Lebkowski, J and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 560)
CN422262 542 bp mRNA linear EST 16
17000424524143 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760
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Section on Molecular Structure and Function
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6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rbrandenberger@geron.com
Insert Length: 542 Std Error: 0.00.
Location/Qualifiers
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Mol. Vis. 8 (4), 171-184 (2002)
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/db_xref="taxon:9606"
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CD675630.1 GI:32177361
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Homo sapiens
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                                                                                                           KEYWORDS
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/cell lipe="SNU-520"
/lab host="Topilor"
/colne lib="S21SNU520"
/lone lib="S21SNU520"
/clone lib="S21SNU520"
/clone lib="S21SNU520"
/clone lib="S21SNU520"
/clone lib="S21SNU520"
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Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR is site by treatment of TA RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli TopiOf' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                    BM857244 10-amb. 10-amb. 10-amb. 2002 St. 06-MAR-2002 K-EST0141477 S21SNU520 Homo sapiens cDNA clone S21SNU520-78-F09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 503)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: Kim YS

Genome Research Center

Genome Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9606"
/clone="S21SNU520-78-F09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .503
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 78 row: F column: 09
High quality sequence stop: 503.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Stomach"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTCTCCATCTCCGATTC 128
                            494 GGTCTCCATCTCCGATTC 477
  GGTCTCCATCTCCGATTC 18
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                                                                                                                                                                                                                                                                      BM85724
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source

FEATURES

145

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Matches

RESULT 13 CN422262/c

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Gaps

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/tissue type="Lens"
/dev stage="Adult"
/dev stage="Adult"
/dev stage="Adult"
/done lib="Human Lens cDNA (Normalized): fs"
/clone lib="Human Lens cDNA (Normalized): fs"
/clone lib="Human Lens cDNA (Normalized) to human lens
library (by) was normalized by self-aubtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(COC 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA ser-circles were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Gore eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 571)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   571 bp mRNA linear EST 18-MAY-200
EST357116 tomato fruit mature green, TAMU Lycopersicon esculentum
cDNA clone cLEF44P15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center(NISC)."
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 6; Length 560; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
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Generation of ESTs from tomato fruit tissue
Fax: 301 496 0078

Baal: graeme@helix.nih.gov
Plate: 25 row: h column: 07
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1. 560
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
                                                                                                                                                                                           mol_type="mRNA"
db_xref="taxon:9606"
clone="fs25h07"
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KEYWORDS
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/dev_stage="mature green (3-5 days pre-ripening)"
/lab host="SOLR"
/clone_lib="tomato fruit mature green, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site_2:
Xho1; cLEF - Fruit were tagged at the Icm stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
pericarp"
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ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 571; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

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Oy 1 GGTCTCCATCTCCGATTC 18

Db 104 ddrcrcchrcrcchrc 121

Search completed: February 5, 2005, 08:11:49 Job time : 2147.2 secs

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Sequence Sus scrof

Ovis arie

Sequence:

on:

Run

Searched:

Database

Result

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AY005131 Oryctolag
BD084108 Method of
BD102202 Method fo
BT007208 Homo sapi
BT008248 Synthetic
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                                                                                                                                    AR371662 Sequence AR3810913 Sequence Z23116 H.sapiens b AX127722 Sequence AX001203 Sus scrof AF164517 Ovis arie AR054021 Sequence AR12452 Sequence AR172594 Sequence AR172594 Sequence BD243042 Antisense CQ765842 Sequence
                                                                                        AF216205 Sus scrof
U72398 Human Bcl-x
                                                                                                              AR054022 Sequence
AR172595 Sequence
I52012 Sequence 7
AR371662 Sequence
 CQ298444 Sequence
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PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide inhibitors of bcl-xL
Patent: JP 2002519048-A 10 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
S Artificial Sequence
PN 2002519048-A/10
PD 02-JUL-1909 JP 2000557839
PF 02-JUL-1999 US 09/109614
            CQ335104 BD097037
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Location/Qualifiers
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100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide inhibitors of bcl-xL. BD255158
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BD102202
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AR118504
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1 (bases 1 to 18)
Stein, C.A.
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synthetic construct
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AUTHORS
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CQ152574
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CQ250961
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AF245488
AF245489
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                           4526729 segs, 23644849745 residues
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
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18
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AF245487 541 bp mRNA linear MAM 11-APR-2001
Bos taurus clone 1.1 anti-apoptotic regulator Bc1-xL mRNA, partial
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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    (bases 1 to 541)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Direct Submission
Submitted (15-MAR-2000) Unitat de Genetica, Facultat de
Submitted Universitat Autonoma de Barcelona, Campus U.A.B.,
Bellaterra, Barcelona 08193, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
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PE Corporation (NY) (US)
Location/Qualifiers
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                                                                                                   1. .391
/organism="Bos taurus"
                                                                                                                                                                                                  1. .391
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/note="processed"
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PR 02-JUL-1999 US 09/109614
PI CY A STEIN
PC CL2NIS,09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/48,A61K48/00,A61P35/00,C12NIS/00
CC ANTISENSE OLIGONUCLEOTIDE
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIATE LINKAGE
CC PHOSPHOROTHIATE (1) (4)
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Bos taurus clone 2.1 processed bcl-xLp2 pseudogene, complete
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Amills, M. and Bouzat, J.
Characterization of the bovine bcl-xL gene and related pseudogenes
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Oligonucleotide inhibitors of bcl-xL
Oligonucleotide inhibitors of bcl-xL
Datent: JP 2002519048-A 29 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
N JP 2002519048-A/29
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                                                                                         Oligonucleotide inhibitors of bcl-xL. BD235177
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02-JUL-1999 JP 2000557839
02-JUL-1998 US 09/109614
CY A STEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic co
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misc_binding (15)..(
Location/Qualifiers
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    CCTGGGGTGATGTGGAGC 18
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JP 2002519048-A/29.
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Amills, M. and Bouzat, J.
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artificial sequences.
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FEATURES

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                                                                                                                                                                                                                                                           AF245489 541 bp mRNA linear MAM 11-APR-2001
Bos taurus clone 1.3 anti-apoptotic regulator Bcl-xL mRNA, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characterization of the bovine bcl-xL gene and related pseudogenes Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (15-MAR-2000) Unitat de Genetica, Facultat de
Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B.,
Bellaterra, Barcelona 08193, Spain
Location/Qualifiers
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  /codon start=1
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  /db_xref="G1:1359160"
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                                         Score 18; DB 4; I
Pred. No. 1.5e+02;
; Mismatches 0;
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llarity 100.0%; Pred. No. 1.5e+02;
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Amills, M. and Bouzat, J.
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NRWFLTGWTVAGVVLLGSLF"
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NRWFLTGMTVAGVVLLGSLF"
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Bos taurus clone 1.2 anti-apoptotic regulator Bcl-xL mRNA, partial
                  Characterization of the bovine bcl-xL gene and related pseudogenes Unpublished
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Amills,M. and Bouzat,J.
Characterization of the bovine bcl-xL gene and related pseudogenes
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                      2 (bases I to 541)
Amills, M. and Bouzat, J.
Direct Submission
Submitted (15-MAR-2000) Unitat de Genetica, Facultat de
Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B.,
Bellaterra, Barcelona 08193, Spain
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Amills, M. and Bouzat, J.
Direct Submission
Submitted (15-MAR-2000) Unitat de Genetica, Facultat de
Veterinaria, Universitat Autonoma de Barcelona, Campus U.A.B.
Bellaterra, Barcelona, 08193, Spain
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/clone="1.2"
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Amills, M. and Bouzat, J.
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Fenn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER-130 - PB 0004 WO
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BE207063.1, EVALUE 0.00e+00~NT HIT: U72398.1, EVALUE
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- 1.7-SWISSPROY HIT: 007817, EVALUE 1.00e-106-EST HUMAN
HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
Patent: WO 0157274-A 17227 09-AUG-2001;
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Larity 100.0%; Pred. No. 1.5e+02;
Conservative 0; Mismatches 0;
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Sequence 21738 from Patent WO0157277.
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/organism="Homo sapiens"
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Location/Qualifiers
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/db xref="taxon:8606"
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db xref="taxon:9606"

/note="MAP TO AL117381.9-EXPRESSED IN BONE MARROW, SIGNAL

- 4.0-SWISSPROT HIT: 007817, EVALUE 1.00e-106-EST HUMAN

HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta Patent: WO 0157272-A 22554 09-AUG-2001;
Aeomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 22596 09-AUG-2001;
Aeomica, Inc. (US)
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/organism="Homo sapiens"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 9498 09-AUG-2001;
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BE207063.1, EVALUE 0.00e+00-NT HIT: U72398.1, EVALUE
                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful analysis of gene expression in human brain Patent: WO 0157275-A 21867 09-AUG-2001;
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HIT: BE207063.1, EVALUE 0.00e+00-NT HIT: U72399.1, EVALUE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
Patent: WO 0186003-A 21963 15-NOV-2001,
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human fetal liver
Patent: WO 0157277-A 21738 09-AUG-2001;
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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1 cctggggtgatgtggagc 18 IDENTITY NUC Scoring table: Sequence:

4134886 segs, 2624710521 residues Gapop 10.0 , Gapext 1.0 Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 sed 0B 0B Minimum I Maximum I

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz46980 Bcl-Xl mR	Aba73433 Human foe	Aai53868 Probe #22	Aba38761 Probe #17	Aak48039 Human bon	Aak21876 Human bra	Abs47753 Human liv	Abs21972 Human gen	Ach87595 Human gen	Aba60917 Human foe	Aai40812 Probe #94	Aba28894 Probe #73	Aak35096 Human bon	Aak09207 Human bra	Abs34848 Human liv	Abs09558 Human gen	Aah48169 Mutant bc	Aah43464 cDNA clon	Adm45994 Human apo	Aag81699 Human thy	Abz83507 Toxicolog
SUMMARIES	ID	AAZ46980	ABA73433	AA153868	ABA38761	AAK48039	AAK21876	ABS47753	ABS21972	ACH87595	ABA60917	AA140812	ABA28894	AAK35096	AAK09207	ABS34848	ABS09558	AAH48169	AAH43464	ADM45994	AAQ81699	ABZ83507
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Adi32132 Human cDN Adg65218 Human Bcl Aaf30926 Human Bcl Adg65209 Human Bcl	Aaq81698 Human thy Aat40079 Bcl-xL ge Aa293614 Bcl-x gen Aa815189 Human bcl Aac90810 Human Bcl Abk84766 Human CDN	Abd16641 Human bc1 Add56479 Human bc1 Add64187 Human bc1 Add3132104 Human cDN Adh52630 Human ach Adh52630 Human arc	Adp13351 Renal cel Aas00247 BC1-XI-DT Aas00250 LFn-Bc1-X Adg89403 Cancer de Adn04260 Antipsori Ado19866 Human PRO Aax33182 Base sequ Ach46093 Human inf
1 ADI32132 2 ADG65218 AAF30926 2 ADG65209	AAQ81698 AAT40079 AAZ93614 AAZ15189 AAC90810 ABK84766	ABT16641 0 ADD56779 0 AAD64187 1 AD132104 2 ADH52630 2 ADO19990	AAS00247 AAS00247 AAS00250 0 ADG89403 2 AD004260 2 AAX33182 ACH46093
737 1 739 1 747 4	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	926 926 926 926 1	926 1 1236 5 1455 5 2386 1 25575 1 7372 2
100.0 100.0 100.0	110000000000000000000000000000000000000	1000.000000000000000000000000000000000	100.0 100.0 100.0 100.0 100.0 100.0
18 18 18 18		100000000000000000000000000000000000000	18 18 18 18 18 16.4
C 23 C 24 C 24	C 26 C 27 C 28 C 29 C 30	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Bcl-X1 mRNA specific antisense oligo J. AAZ46980 standard; DNA; 18 BP 98US-00109614. 99WO-US015250. (first entry) WO200001393-A2. 02-JUL-1999; Homo sapiens. 02-JUL-1998; 14-APR-2000 13-JAN-2000. AAZ46980; AAZ46980

(UYCO) UNIV COLUMBIA NEW YORK.

Stein CA;

WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English

The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour cells to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                   Probe #22554 used to measure gene expression in human placenta sample
                                                                                                                                                             microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060B40B.
03-AUG-2000; 2000US-00346B7P.
21-SEP-2000; 2000US-02346B7P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000663
                                                       AAI53868 standard; DNA; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53.
                                                                                                                                                                         genetic disorder;
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                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                          04-FEB-2000;
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                                                                                                        17-OCT-2001
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                                                                                                                                                             Probe;
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                          RESULT 3
                                         AAI53868
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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-X1 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                           100.0%; Score 18; DB 3; Length 18; 100.0%; Pred. No. 58;
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                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                     Human foetal liver single exon nucleic acid probe #21738.
                                                                  Sequence 18 BP; 2 A; 3 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression in human fetal liver.
                                                                                                                                                                        18
                                                                                                                                                                                                                                          ABA73433 standard; DNA; 555 BP.
                                                                                                                                               1 CCTGGGGTGATGTGGAGC 18
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2000US-0207456P.
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2000US-0236359P
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                                                                                                                                                              CCTGGGGTGATGTGGAGC
                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                      18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52
                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 18; Conserv
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21-SEP-2000;
27-SEP-2000;
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ID ABA7
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DR; Rank

Chen W,

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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe #17227 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                       DB 4; Length 555;
65;
                                                                                                                                                                           Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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Claim 25; SEQ ID NO 22554; 654pp; English.
                                                                                                                                                                                                                       100.0%; Score 18; 100.0%; Pred. No. (
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Les 18; Conservative
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CCTGGGGTGATGTGGAGC 232

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CCTGGGGTGATGTGGAGC 18

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 22596; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
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Pred. No. 65;
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100.0%;
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408
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                                                                                                                                                                                                                                                                                                                                                                                                               the probes of the invention
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Best Local Similarity 100.
                                                                                                                                                   Hanzel DK,
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                                                                                                                                                                                        WPI; 2001-488900/53
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30-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 17227; 530pp; English.
                                                                                                                                                                                                                                                                                                                                     Rank DR
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408.
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26-MAY-2000; 2000US-0207456P.
                                                                                                          30-JAN-2001; 2001WO-US000666
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488899/53
                                    WO200157274-A2
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Homo sapiens.
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RESULT 5

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Gaps ö liver single exon nucleic acid probes of the invention. Note: The

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                          probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                Gaps
                                              present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss.
             4; SEQ ID NO 21867; 650pp + Sequence Listing; English.
                                                                                                                                                                                                               100.0%; Score 18; DB 4; Length 555; 100.0%; Pred. No. 65;
                                                                                                                                                                              Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                0; Mismatches
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2000US-00632366.
2000US-0234687P.
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2000GB-00024263.
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Best Local Similarity
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                 invention
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               Example
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ABS47753
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                                at
            sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicoytosis; lymphangioleiomyomicosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
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Mismatches
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                                                                                                                  100.0%; Score 18;
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408.
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nes 18; Conservative
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30-JUN-2000;
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Matches
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array; identifying exons in a eukaryotic ganome, comprising (a) array; identifying exons in a eukaryotic ganome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method bove and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, a peptizing one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung these exercities in the such as asthma. The probes of the such as asthma, lung cancer, chronic sclerosis, Gaucher's disease, Namman-Pick disease, Hermansky-tuberous sclerosis, Jumpanany planemary alvealar primary criarary ciliary arrians contributed by the contributed by pulmonary has primary criarary criarary criarary criarary criarary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karagemer syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   and (b) measuring the label detectably bound to each probe of the
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Gaps ; 0 100.0%; Score 18; DB 6; Length 555; 100.0%; Pred. No. 65; 0; Indels Mismatches ; 1 CCTGGGGTGATGTGGAGC 18 Local Similarity 100. nes 18; Conservative Query Match Matches 8

Sequence 555 BP; 105 A; 178 C; 139 G; 133 T; 0 U; 0 Other;

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215 cerecedraterenace 232 셤

ACH87595 standard; DNA; 564 BP (first entry) 29-JUL-2004 ACH87595; ACH87595

Human genome derived single exon probe #20790.

Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.

Homo sapiens

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Hanzel DK; Rank DR, Penn SG,

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-cadressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid of probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a wector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above.

The plant of a peptide control of a peptide cited above.

The plant of a peptide control of a period above. methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing towand selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe crited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their genetic exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising calternative splicing events, in detecting and characterising gross alternations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the order encoded peptide. The present sequence is a human single exon probe of the invention, Note: The sequence is a human single exon probe of the invention. Note: The sequence is a human single exon probe of the invention. ö patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at Gaps splicing events, for assessing genomic alterations or as tools for ö 100.0%; Score 18; DB 12; Length 564; 100.0%; Pred. No. 65; Seguence 564 BP; 108 A; 180 C; 141 G; 135 T; 0 U; 0 Other; Indels segdata.uspto.gov/sequence.html?DocID=20030194704 .. 0; Mismatches Claim 1; SEQ ID NO 20790; 80pp; English Local Similarity 100. nes 18; Conservative surveying tissues. Query Match Matches

CCTGGGGTGATGTGGAGC 232 1 CCTGGGGTGATGTGGAGC 18

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ABA60917 standard; DNA; 600 BP. (first entry) 01-FEB-2002 ABA60917; RESULT 10 ABA60917

Human foetal liver single exon nucleic acid probe #9222.

Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

Homo sapiens

WO200157277-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000669.

04-FEB-2000; 2000US-0180312P

us-09-753-169a-10.rng

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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
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         30-JUN-2000; 2000US-00608408.
03-MG-2000; 2000US-0053336.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408.
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21-SEP-2000; 2000US-0234687P,
27-SEP-2000; 2000US-0236359-
04-OCT-2000; 2000GB-00054263
 2000US-0207456P
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Best Local Similarity 100.00
Conservative
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                                                                                                                Penn SG, Hanzel DK,
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WPI; 2001-488897/53

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                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                 Claim 25; SEQ ID NO 9498; 654pp; English.
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gene expression in human placenta.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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RESULT 13 AAK35096

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1 expressed exon; gene expression analysis; probe; microarray;
disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, single exon nucleic acid probe, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hyperlipidaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 9198; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 18; DB 4; Length 600; 100.0%; Pred. No. 65; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
                                                                                                     Juman brain expressed single exon probe SEQ ID NO: 9198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human liver single exon probe, SEQ ID No 9838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGGGGTGATGTGGAGC 251
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   AAK09207 standard; DNA; 600 BP.
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-02359P.
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                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000667
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Matches 18; Conser
                                                                                                                                                                                                                                         WO200157275-A2
                                                                                                                                     brain
                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                         Alzheimer's
                                                                     35-NOV-2001
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                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed single exon probe SEQ ID NO: 9653.
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                                                                     Length 600;
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                                 Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 100.0
warehes 18; Conservative
                                                            Query Match
Best Local Similarity 100.
Matches 18; Conservative
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27-SEP-2000;
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30-JUN-2000;
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Gaps

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coronary heart disease; ss

Homo sapiens

RESULT 14 AAK09207

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 18; DB 4; Length 600; Best Local Similarity 100.0%; Pred. No. 65; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 600 BP; 116 A; 184 C; 152 G; 148 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 9838; 658pp; English.
                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456F.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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                                                                                              30-JAN-2001; 2001WO-US000664
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                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488898/53
                WO200157273-A2
                                                       09-AUG-2001
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Search completed: February 4, 2005, 21:52:43 Job time : 232.23 secs 234 CCTGGGGTGATGTGGAGC 251 g

1 CCTGGGGTGATGTGGAGC 18

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Gaps ö

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F08773 HSC25B061 IN B1395503 M.P-P-AX1-B109503 M.P-P-AX1-B1060608 IL3-UT011 AZ576742 AST-2T009 B1051278 CW3-GW01420 CW3-GW01420 Z37460 LT HP-CB0 W01420 Z37460 LT HP-CB0 BM857244 K-EST0141 H09884 YM05507 LT CW42252 170004245 CW422561 170004245 CW422561 170004245 CW422561 170004245 CW422561 170004245 CW422562 170004245 CW422562 170004245 CW422562 170004245 CW422562 170004245 CW42252 170004245 CW42252 170004245
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BE818722 PM3-BN030
                                                                                     2005, 20:41:45; Search time 2146.2 Seconds (without alignments) 305.616 Million cell updates/sec
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5.1.6
Compugen Ltd.
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 GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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18
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seq length: 200000000
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B1960951 MONO1 3 A CB448211 702275 MA BE783664 601471247

BE871836 BI960951 CB448211 BE783664

7 CN422264 170005326 7 2 BE207063 BE207063 7 CK832794 ANB14739 MR1-6705.Y 7 CK832794 4056433 B 7 CK832794 4056433 B 8 BE293685 601186941 B 9 4 BICTORES BG708652 601186941 9 4 BICTORES BG708652 602185360 9 4 BICTORES BG81020 603185360 9 4 BICTORES BG81020 601447403 9 4 BICTORES BG810269 601447403 9 4 BICTORES BG201262 60218526193 9 4 BICTORES BG201262 602156193 1 4 BICTORES BG201262 60218627 1 4 BICTORES BG201262 60218627 1 4 BICTORES BG201262 50421144 1 4 </th <th>ALIGNMENTS</th> <th>BE771987 CM3-FT0100-140700-245-e05 FT0100 Homo sapiens CDNA, mRNA sequence. BE771987.1 GI:10225645 EST7.1987.1 GI:1025645 Homo sapiens ENARTYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R., Magali,M.A., Garcia,M.A., Bordin,S., Costa,P.F., Brunstein,A., Geoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Harse,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and</th> <th>Subgroun, A.J Shipson, A.J Shipson, A.J Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Broce. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663 10737800 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,</th> <th>m the FAPESP/LICR en in the followi ipts/gethtml2.pl? 1) 9. ens" " te_tumor; Vector: -IIbrary was made S PCR (U.S. Lette</th>	ALIGNMENTS	BE771987 CM3-FT0100-140700-245-e05 FT0100 Homo sapiens CDNA, mRNA sequence. BE771987.1 GI:10225645 EST7.1987.1 GI:1025645 Homo sapiens ENARTYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R., Magali,M.A., Garcia,M.A., Bordin,S., Costa,P.F., Brunstein,A., Geoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Harse,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and	Subgroun, A.J Shipson, A.J Shipson, A.J Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Broce. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663 10737800 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,	m the FAPESP/LICR en in the followi ipts/gethtml2.pl? 1) 9. ens" " te_tumor; Vector: -IIbrary was made S PCR (U.S. Lette
18 100.0 632 19 100.0 657 19 100.0 675 19 100.0 687 19 100.0 688 100.0 689 118 100.0 699 118 100.0 705 118 100.0 705 118 100.0 716 118 100.0 716		BE771987 CM3-F70100-140700-24 BE771987.1 GI:10225 BE771987.1 GI:10225 Homo sapiens (human) Homo sapiens (human) Homo sapiens To Manalia; Eutheria; 1 (bases I Eutheria; 1 (bases I, Garcia Mammalia; Eutheria; 1 (bases I, Garcia Manalia; Eutheria; 1 (bases I, Garcia Manalia; Eutheria; 1 (bases I, Garcia Manalia; Garcia Manalia; Garcia Manalia; H., Garvai Goldman, G. H., Carvai Brunstein, A., deolii, Cimacon, A., Soares,	Simplent, A.J. Subtyun sequencing of sequence tags Proc. Natl. Acad. Sci. 20202663 10737800 Contact: Simpson A.J.G Laboratory of Cancer G Ludwig Institute for C Ludwig Institute for C Ludwig Institute for C	Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived fro Project. This entry can be se (http://www.ludwig.org.br/scr 7700-245-e05&13-2000-07-14&kt4- 849 quality sequence stop: 6 Location/Qualifiers 1. 161 /organism="Homo sapi//db_xref="#axon:9006/dev_etage="#axon:9006"#axon:9006/dev_etage="#axon:9006"#axon:9006/dev_etage="#axon:9006"#axon:9006/dev_etage="#axon:9006"#axon:9
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Query Match

ORIGIN

Matches

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 2 BE818722/c

SOURCE ORGANISM

REFERENCE AUTHORS

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/tissue type="total brain"
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/dev_stage="3 months old"
/dev_stage="3 months old"
/clone lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; cotal mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
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BI399503.1 GI:15178564
                                                                                                                                                                                                                                                               F08773 20-FEB-1995
HSC25B061 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotti Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 29)
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Sebastiani-Kabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genexpress_library_idt: C; Genexpress_sequence_idt: y3c-25b06
Seq primer: (-21)M13_universal.
_Location/Qualifiers
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1, rue de l'Internationale, BP60 91002 BVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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/db_xref="taxon:9606"
/clone="c-25b06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genexpress@genethon.fr
Single read.
                                                     190 CCTGGGGTGATGTGGAGC 173
               1 CCTGGGGTGATGTGGAGC 18
                                                                                                                                                                                                                                                                                                                                            c-25b06, mRNA sequence.
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Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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VERSION
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BI399503
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No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ыжыв 1722 21-SEP-2000
РМЗ-ВN0300-080700-002-g11 BN0300 Homo sapiens CDNA, mRNA sequence.
BE818722
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1 (Dases I to 294)

1 (Dases I to 294)

1 (Dases I to 294)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Rax: +55-11-2707001
Exa: +55-11-2707001
Exa: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entery can be seen in the following URL (http://www.ludwig.org.br/esripts/gethtml2.pl?tl=&t2=PM3-BN0300-080700-002-911&t3=2000-07-08&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                             100.0%; Score 18; DB 2; Length 161; 100.0%; Pred. No. 5.6e+02;
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/organism="Homo sapiens"
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High quality sequence start: 33
High quality sequence stop: 294.
Location/Qualifiers
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0300"
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/mol Lype="mark" saptems //mol Lype="mark" mark //mol Lype="mark" mark //mol Lype="mark" mark //mol Lype="mark" mark //mole="drgam: uterus tumor; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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                                                                                                                                                                                                                                                                                                                                                Email: asimpsonoludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0115-
300101-433-803&t2=25001-01-30&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 310.
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Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                               sequence tags
Proc. Natl. Acad: Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Exon-trap tags from a T47D GenomeScreen(TM) Library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 310;
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llarity 100.0%; Pred. No. 5.9e+02;
Conservative 0; Mismatches 0;
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11010 Torreyana Road, San Diego,
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AZ576742.1 GI:11563053
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                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Brazil
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AUTHORS
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KEYWORDS
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/lab_host="NH10B (Life Technologies)"
/clone=lib="NH10B (Life Technologies)"
/clone=lib="NH10B (Life Technologies)"
/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AY1
library is normalized library derived from the MI-P-AY0
library ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.iastate.edu/. The procedure used to
create this library has been previously described
(Ronaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 5152942401
Email: ckutuggle@iastate.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa distribution: clones will be available
through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 bp mRNA linear BST 15-JUN-2001 IL3-UT0115-300101-433-B03 UT0115 Homo sapiens cDNA, mRNA sequence. B1060608.1 GI:14468135 EST.
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1 (bases 1 to 310)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Cetartiodactyla, Suina, Suidae, Sus. 1 (bases 1 to 305)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
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/strain="crossbreed"
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                       scrofa (pig)
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BI060608
KEYWORDS
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1 (Dases I to 418)

2 (Dase I to 418)

3 (Dase I to 418)

4 (Dases I to 418)

5 (Dase I to 418)

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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-
110101-607-60&ts1=2001-01-11&t4=1)
Beq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 418.
Location/Qualifiers
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CM3-GN0297-110101-607-£03 GN0297 Homo sapiens cDNA, mRNA sequence.
BIO51278
proceeded by a splice acceptor as a reporter for gene expression, 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DHS-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.

Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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/db_xref="taxon:9606"
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/cell_line="T470"
/clone_lib="Genetrap T470 Human Breast Carcinoma Ince="Togan: Breast; Vector: pAmp-1; 3' RACE of from genetrap pools; shocgun clone in pAmp-1 and transform DHS-alpha competent bacteria."
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20202663
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/mol_type="mRNA"
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Matches 18; Conservative
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/tissue type="Lymph node"
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/lab_host="Topl0F"
/clone_lib="S12SNU216"
/lone="Topl0F"
/clone_lib="S12SNU216"
/clone_li
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K-EST0122378 S12SNU216 Homo sapiens cDNA clone S12SNU216-63-B03 5',
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1 (bases 1 to 421)
1 (bases 1 to 421)
2 (bases 1 to 421)
3 (bases 1 to 421)
6 (by N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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/note="Cycan: placenta_normal; Vector: puc18; Site_1:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 186,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-866-44710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 418;
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100.0%; Pred. No. 6e+02;
ive 0; Mismatches 0
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Unpublished (2002)
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/clone="S12SNU216-63-B03"
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Email: yongsung@mail.kribb.re.kr
Plate: 63 row: B column: 03
High quality sequence stop: 421.
Location/Qualifiers
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nes 18; Conserv
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셤 8

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/mol_type="mRNA"
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/clone="taxon:9606"
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/clone lib="soares"
/clone lib="s
                                                                                                                                                                                                                                  W01420 tan 10 437 bp mRNA linear EST 18-APR-1996 za73d06.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:298187 5' sīmilar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
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1 (Dases I to 437)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infloginage.llnl.gov) for further information. Seq primer: mob.REGA+ET High quality sequence stop: 383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                               BCL-X.;, mRNA sequence.
W01420
W01420.1 GI:1273428
          1 CCTGGGGTGATGTGGAGC 18
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Best Local Similarity
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W01420/c
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/tissue types:305909.7
/lab host="DH10B (T1 phage resistant)"
/lab host="DH10B (T1 phage resistant)"
/clone_lib="NIH MGC_210"
/slone_lib="NIH MGC_210"
/note="Organ: Prostate; Vector: pT7T3 Pac; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratlift."
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UI-HF-CB0-asn-f-06-0-UI.rl NIH_MGC_210 Homo sapiens CDNA clone
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competent cells B. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
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                                                                                                                                                                   100.0%; Score 18; DB 4; Length 421; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
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clone="IMAGE:30569057"
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CF145335/c
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/mol_type="mRNA"
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High quality sequence start: 41
High quality sequence stop: 475
Location/Qualifiers
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Location/Qualifiers
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    Contact: Brandenberger
                         Regenerative Medicine
Geron Corporation
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Best Local Similarity 100.
Matches 18; Conservative
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BQ331598/c
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                                                                                                                                                                                                                                                                                                                                                                                             Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TW) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Prostate; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and use to transform DHS-alpha competent bacteria."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Library"
                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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17000424524125 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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                                                                                                                                                                          1 (bases 1 to 456)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M.,
Bernardino,A., Durick,K. and Pollok,B.
Exon-trap tags from a PC-3 GenomeScreen(TM) Library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 18; DB 8; Length 456; 100.0%; Pred. No. 6e+02;
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11010 Torreyana Road, San Diego, CA 92121, USA
sapiens genomic 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="genomic DNA"
/db_xref="taxon:9606"
/tiseue_type="Adenocarcinoma"
/cell_type="Richelial"
/cell_line="PC-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                    AZ537061
AZ537061.1 GI:11113828
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                                                                                                                                                                                                                                                                                      Contact: Greg Henkel
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                                                                                                              Homo sapiens
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/tissue type="mbryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone lib="GRN BB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 475)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O', Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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MR4-ET0138-080501-010-d06 ET0138 Homo sapiens cDNA, mRNA sequence.
BQ331598.1 GI:20972765
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=WR4&t2=MR4-ET0138-
080501-010-d06&t3=2001-05-08&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 474;
230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Exes: 650 473 776 Email: Exhandenberger@geron.com Insert Length: 474 Std Error: 0.00.
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sequence tags
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1 MGC_42"
/clone_lib="NH1 MGC_42"
/note="Organ: nH1 MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: ECoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the birectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: agGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM050133 478 bp mRNA linear EST 07-NOV-2001
600532480F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5422338 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCWH879 row: p column: 19
High quality sequence stop: 267.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Exausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                   100.0%; Score 18; DB 5; Length 475; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                          CCTGGGGTGATGTGGAGC 225
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                                                                                                                                                                                                                                                         llarity 100.0%;
Conservative (
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Matches 18; Conservative
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BM050133/c
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Gaps

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100.0%; Score 18; DB 4; Length 478; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels

0; Mismatches

1 CCTGGGGTGATGTGGAGC 18

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
1 (bases I to 486)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR1-ST0206-120 Seq primer: puc 18 forward
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MRI-ST0206-120400-022-£04 ST0206 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/organism="Homo sapiens"
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Job time : 2148.2 secs
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High quality sequence stop: 485.
Location/Qualifiers
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/db_xref="taxon:9606"
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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AR054021 Sequence
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PI CY A STEIN
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Patent: JP 2002519048-A 11 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OF Artificial Sequence
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/organism="synthetic construct"
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02-JUL-1999 JP 2000557839
02-JUL-1998 US 09/10961
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Patent: JP 2002519048-A 31 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
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PN JP 2002519048-A/31
PD 02-JUL-1990 JP 2000557839
PP 02-JUL-1999 US 09/109614
PI CY A STEIN
PC CLINIS/09,A61K9/127,A61K9/51,A61K31/711,A61K31/7125, PC
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.6e+02;
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    .387
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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A61K47/42,

PC A61K47/42,

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Patent: JP 2002519048-A 30 02-JUL-2002;
PTHE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/30
PD 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
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                                                                                                                   BD235178
Oligonucleotide inhibitors of bcl-xL.
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JP 2002519048-A/30.
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synthetic construct
artificial sequences.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN HEART, SIGNAL = 1.6"
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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MAILYSTS OF GENE EXPRESSION IN HUMAN ADULT LIVERS.130. PB 0004 WO 3<br/>
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150.0 US 60/180, 312.151.0 04 February 2000 (04.02.00)<br/>
60/207, 456<br/>
150.00 (03.08.00)<br/>
170.00 (03.08.00)<br/>
170.00 (10.08.00)<br/>
170.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0157274-A 6802 09-AUG-2001;
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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Location/Qualifiers
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Matches 18; Conserv
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CQ221990
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN PLACENTA, SIGNAL =
1.5"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 8597 09-AUG-2001;
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human placenta
Patent: WO 0157272-A 8448 09-AUG-2001,
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CQ138575.
CQ138575.1 GI:41095941
                                                                                                                                                 CQ099589 Sequence 8448 from Patent WO0157272.
CQ099589
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/organism="Homo sapiens"
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1. .587
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/noTe="MAP TO AL117381.9~EXPRESSED IN BRAIN, SIGNAL = 2"
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleaic acid probes useful for analysis of gene expression in human brain Patent: WO 0157275-A 8152 09-AUG-2001;
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synthetic construct
artificial sequence.

a trificial sequence.

S Shimizu, S. and Tsujimoto, Y.

A BH4 fusion polypeptide

L Satent: WO 0148014-A 3 05-JUL-2001;
SHIONOGI & CO LTD, SHIGEOMI SHIMIZU, YOSHIHIDE TSUJIMOTO
OS Artificial Sequence
PN WO 0148014-A/3
PD 05-JUL-2001
PF 26-DEC-2000 WO 2000JP009274
PR 27-DEC-1999 JP 99P 371449
PR SPICEC-1000 A 2000JP009274
PR SPICEC-1000
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
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                                                                  Sequence 8152 from Patent W00157275.
CQ334058
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human fetal liver
Patent: WO 0157277-A 8196 09-AUG-2001;
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
Patent: WO 0186003-A 8816 15-NOV-2001;
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/db_xref="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN LUNG, SIGNAL =
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Sequence 8196 from Patent WO0157277.
CQ259935
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CQ297711
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/organism="Homo sapiens"
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I (bases 1 to 702)
Kato, S., Eguchi, C. and Nagata, N.
Method of detecting protein-protein interaction
Batent: JP 2001327296-A 7 27-NOV-2001,
JAPAN SCIENCE AND TECHNOLGY CORP
OS Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                             24-AUG-2000 JP 2000254418
SEISHI KATO, CHIKASHI EGUCHI, NAOKI NAGATA
CI2N15/09,C12Q1/02//C07K14/47, (C12N15/09,C12R1:91), (C12Q1/02,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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PR 15-MAR-2000 JP 00P 073095,24-AUG-2000 JP 00P 254418 PI SEISHI KATO,CHIKASHI EGUCHI,NAOKI NAGATA,MIYAKO OTAKE PC C12N15/79,G011031/68//C12P21/02,C07K19/00
CC Method for detecting protein-protein interaction FH Key Location/Qualifiers
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C12N15/00, (C12N15/00, C12R1:91)
Method of detecting protein-protein interaction FH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        702 bp DNA linear Method for detecting protein-protein interaction. BD102202
                                                                        Method of detecting protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kato, S., Eguchi, C., Nagata, N. and Otake, M. Method for detecting protein-protein interaction Patent: WO 0168885-A 7:20-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .702
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . (702).
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAGATA, MIYAKO OTAKE
OS Homo sapiens (human)
PN WO 0168885-A/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 AGTICCACAAAAGTAICC 501
                                                                                                                                   BD084108.1 GI:22629718
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WO 0168885-A/7.
                                                                                                                                                                                                                                                                                                                                         JP 2001327296-A/7
27-NOV-2001
                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                    JP 2001327296-A/7
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Best Local Similarity
Matches 18; Conserva
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ACCESSION
VERSION
                                               RESULT 13
BD084108/c
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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SOURCE
ORGANISM
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LOCUS
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AUTHORS
                                                                                                                                                                                                                                                                      TITLE
JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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Unpublished

(bases 1 to 702)

(kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundiny, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length expression clones generated by BB Biosciences Clonnech and the expression clones generated by BB Biosciences Clonnech and the farvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall the clonin sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
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METEBAINGNPSWHIADSPAVNGATCHSSSLDAREVI PMAAVKQALREAGDEFELRYR
RAFSDLTSQLHITPGTAYQAFBQVVNBLFRDGVNWGRIAAFFSFGGALCVESVDKEMQ
VLVSRIAAMMATYLINDHLEPWIQENGGWDTFVGLYGNNAAAESRKGQERFNRWFLTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 702)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,W., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Chen,M., and Farmer,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="BD Creator(TM) CDS Library derived from MGC
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                      Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   702 bp mRNA li
Homo sapiens BCL2-like 1 mRNA, complete cds.
BT007208
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/note="Vector: pDNR-Dual"
                                                                                                                                                                              100.0%; Score 18; DB 6; L
llarity 100.0%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 0;
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/db_xref="GI:30583255"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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product="BCL2-like 1"
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/clone="GH00804X1.0"
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Query Match 100.0%; Score 18; DB 9; Length 702; Best Local Similarity 100.0%; Pred. No. 1.18+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: February 4, 2005, 23:30:42 Job time : 433.664 secs

Op

us-09-753-169a-11.rng

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model	on: February 4, 2005, 15:50:53; Search time 232.23 Seconds (without alignments) 406.880 Million cell updates/sec	Title: Perfect score: 18 Sequence: 1.agttccacaaagtatcc 18 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0	Searched: 4134886 seqs, 2624710521 residues Total number of hits satisfying chosen parameters: 8269772	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	abase : N Geneseq 23Sep04:* 1. geneseqn1980s:* 2: geneseqn1990s:* 3: geneseqn2000s:* 5: geneseqn2001as:* 6: geneseqn2001bs:* 7: geneseqn2002bs:* 8: geneseqn2003as:* 9: geneseqn2003as:* 10: geneseqn203ss:* 11: geneseqn2003cs:* 12: geneseqn2003cs:*
OM nucleic	Run on:	Title: Perfect sc. Sequence: Scoring tal	Searched: Total numb	Minimum DB Maximum DB	Post-proce	Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz46981 Bcl-Xl mR	Ach84269 Human gen	Adk66037 Standardi	Ach46093 Human inf	Aba59891 Human foe	Aai39762 Probe #84	Aba28336 Probe #68	Aak34040 Human bon	Aak08161 Human bra	Abs33839 Human liv	Abs08825 Human gen	Ach70569 Human gen	Aah48169 Mutant bc	Aah43464 cDNA clon	Adm45994 Human apo	Aag81699 Human thy	Abz83507 Toxicolog	Adi32132 Human cDN	Adg65218 Human Bcl	Aaf30926 Human Bcl	Adg65209 Human Bcl
SUMMARIES	OI	AAZ46981	ACH84269	ADK66037	ACH46093	ABA59891	AAI39762	ABA28336	AAK34040	AAK08161	ABS33839	ABS08825	ACH70569	AAH48169	AAH43464	ADM45994	AAQ81699	ABZ83507	ADI32132	ADG65218	AAF30926	ADG65209
	DB	м	12	10	σ	4	4	4	4	4	4	9	12	4	Ŋ	12	N	10	11	12	4	12
	Query Match Length DB	18	179	337	492	587	587	587	587	587	587	587	587	636	702	702	737	737	737	739	747	747
d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18
	Result No.	н	ر 2	ص ن	Ω 4	ហ	9	7	80	6	10	11	c 12	c 13	c 14	c 15	c 16	c 17	c 18	c 19	c 20	c 21

Aaq81698 Human thy Aat40079 Bcl-xL ge Aas19161 Bcl-x gen Aas19189 Human Bcl Abc90810 Human Bcl Abc90810 Human bcl Add56779 Human bcl Add50990 Human Bcl Add13210 Human ant Add19990 Human PRO Adx01990 Human PRO Adx01990 Human PRO Adx01996 Human PRO Adx01986 Human PRO Adx31182 Base sequ Adx31182 Base sequ Aax31182 Base sequ
88 89 99 99 99 99 99 99 99 99 99 99 99 9
AAQ81698 AAT40079 AAA23614 AAA23614 AAA23619 AAC39610 ABK844641 ADB54779 ADB54789 AAC300247 AAC300247 AAC300247 AAC30247 AAC30247 AAC3186 AAC3188 AAC33182 AAC356503 AAC33182 AAC356503 AAC3367
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
72221 72221 72222 72222 72
0.000000000000000000000000000000000000
000000000000000000000000000000000000000
17 17 17 17 17 17 17 17 17 17 17 17 17 1
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

AAZ46981 standard; DNA; 18 BP

RESULT 1

New antisense oligonuclectides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions. Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Bcl-Xl mRNA specific antisense oligo K. (UYCO) UNIV COLUMBIA NEW YORK. 98US-00109614. Claim 1; Fig 1; 69pp; English 99WO-US015250. (first entry) WPI; 2000-137140/12. WO200001393-A2. Homo sapiens. 02-JUL-1999; 02-JUL-1998; 14-APR-2000 13-JAN-2000. AAZ46981; Stein CA;

The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein bcl-xL. The oligonucleotides can be introduced into tumour calls to reduce bcl-xL production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce bcl-xL production to promote the regression of vascular.

George medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of mucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at

999999999999999988

gene expression data by subscription, and a computer-readable

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-X1 mRNA
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                        gene expression; single exon probe; microarray;
                                                                                                         ö
                                                                               100.0%; Score 18; DB 3; Length 18; 100.0%; Pred. No. 21;
                                                                                                        0; Indels
                                                           Sequence 18 BP; 7 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                      Human; probe; ss; gene expression; single exon alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                Human genome derived single exon probe #17464.
                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 17464; 80pp; English.
                                                                                                                                                                                                              ACH84269 standard; DNA; 179 BP.
                                                                                                                              1 AGTICCACAAAAGIAICC 18
                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Rank DR, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-2002; 2002US-00029386
                                                                                                                                             1 AGTTCCACAAAAGTATCC
                                                                                                                                                                                                                                                         (first entry)
                                                                                                        18; Conservative
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                JS2003194704-A1
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                         29-JUL-2004
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                                                                                  Query Match
                                                                                                        Matches
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Gaps

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Indels

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Mismatches

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Local Similarity 100.

Matches

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Query Match

18 20

37 AGTICCACAAAAGTAICC 1 AGTTCCACAAAAGTATCC

100.0%;

Score 18; DB 12; Length 179; Pred. No. 26;

Sequence 179 BP; 37 A; 53 C; 48 G; 41 T; 0 U; 0 Other;

segdata.uspto.gov/sequence.html?DocID=20030194704

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which comprises at least one carrier nucleic acid, at least 3 oligonucleotides, as primers and target-specific, fluorescently labeled probe and optionally at least one set of stabilized controls (standards RNA or DNA) of known concentration and instructions. The system comprises any of 20 sets of one control, two primers and one target-specific probe. The standardized polynucleotide system can be used for quantitative, realtime detection of target nucleic acids, especially analysis of genes or gene products, e.g. for individualized medical diagnosis, in veterinary medicine, functional genomics, clinical pharmacology, pharmacogenetics,
                                                                                                                                                                                ss; standardized polynucleotide system; medical diagnosis;
functional genomics; sample analysis; pharmacogenomics; sample analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Standardized polynucleotide system, useful for quantitative, real-time determination of nucleic acid, comprises stabilized standards, primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a standardized polynucleotide system,
                                                                                                                                                Standardized polynucleotide system polynucleotide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                          (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 7; 38pp; German.
                                                                                                                                                                                                                                                                                                                                                    28-FEB-2002; 2002DE-01009071.
                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2002; 2002DE-01009071.
                                     ADK66037 standard; DNA; 337
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-732912/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koehler T, Rost A;
                                                                                                                                                                                                                                                                             DE10209071-A1.
                                                                                                                                                                                                                                         Unidentified
                                                                                                              06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and probe
                                                                          ADK66037;
                      ADK66037/c
RESULT 3
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expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids dequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of exon microarray for measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above mentioned amino acid

invention relates to a nucleic acid probe for measuring human gene

sequences (optionally with conservative amino acid substitutions), an stoolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing

Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The mucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data con this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. The sequence contained in electronic format directly from USPTO at sequence.
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pharmaceutical testing, analysis of food or environmental samples and also for ultra-sensitive detection of proteins by immuno-PCR. The present sequence is a polynucleotide used in the system of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA libraries, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide sequences obtained from various cDNA libraries, used as hybridization probes, as oligomers for PCR, for chromosome and genemapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                  Gaps
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                                                                                                          100.0%; Score 18; DB 10; Length 337; 100.0%; Pred. No. 27;
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                                                                                                                                                0; Indels
                                                                          Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;
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                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 33305; 44pp; English.
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                                                                                                                                                                                                                                                                                         ACH46093/c
ID ACH46093 standard; cDNA; 492 BP
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                                                                                                                         llarity 100.0%;
Conservative C
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                                                                                                                                                                                  1 AGTTCCACAAAGTATCC
                                                                                                                                                                                                                  178 AGTTCCACAAAAGTATCC
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRMANAC R T.
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                                                                                                  Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The
                                                                                                                                                                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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  Score 18; DB 9
Pred. No. 28;
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2000US-0234687P.
2000US-0236359P.
    100.0%;
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                                                         1 AGTTCCACAAAAGTATCC
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Query Match
Best Local Similarity 100.
Matches 18; Conservative
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nes 18; Conservative
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AAI39762
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AAI39762,

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measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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; 2000US-023459P.
; 2000GB-00024263.
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                                                                       2000US-0207456P.
2000US-00608408.
2000US-00632366.
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2000US-0236359P.
                 30-JAN-2001; 2001WO-US000666
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nes 18; Conservative
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                       Probe #8448 used to measure gene expression in human placenta sample.
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                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023539P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                genetic disorder; ss.
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30-JUN-2000; 03-AUG-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

WO200157274-A2

09-AUG-2001

Homo sapiens

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Query Match Matches ABA28336;

gene expression in brain cell samples,

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                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                               Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                                                                          Example 4; SEQ ID NO 8597; 658pp + Sequence Listing; English.
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                                                                       expression in human bone marrow.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
        MOLECULAR DYNAMICS INC
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                           Hanzel DK,
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es 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
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brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                         4; Length 587;
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                       510 AGTTCCACAAAAGTATCC 527
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coronary heart disease; ss
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                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
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04-OCT-2000;
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                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABS33839;
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having a fragment identical to the predicted exon, the probe is included
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuman lung compitising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes in the human lung, measuring gene expression in a sample acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (b) detecting specific hybridisation of detectably the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
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                                                                                                                                                                                                                                                                                                                                                                Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histiocytosis; Iymphangioleiomyomtosis; Karagener syndrome; pulmonary historofis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spatially-addressable set of single exon nucleic acid probes, used to
                                                           Gaps
                                                                                                                                                                                                                                                                                                        Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                               Human genome-derived single exon probe from lung SEQ ID No 8816.
                                                           ö
                      ch 100.0%; Score 18; DB 4; Length 587; l. Similarity 100.0%; Pred. No. 28; Onservative 0; Mismatches 0; Indels
Sequence 587 BP; 135 A; 129 C; 193 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 8816; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                       510 AGTTCCACAAAAGTATCC 527
                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                      1 AGTTCCACAAAAGTATCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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30-JUN-2000; 2000US-00608408
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                                                                                                                                                                                          ABS08825 standard; DNA; 587
                                                                                                                                                                                                                                                  (first entry)
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                                         sest Local Similarity
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                                                                                                                                                                                                                     ABS08825;
                            Query Match
                                                                                                                                                           Matches
                                                                                                                요
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in the above mentioned microarray; profits assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the coposes, open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (LID), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-histicotycosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, karagener syndrome, fibrocystic pulmonary displasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The sequence data for this patent did not form part of the printed sequence data for this patent did nelectronic format directly from MIPO specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome derived single exon probe #3764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 18; DB 100.0%; Pred. No. 28;
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Best Local Similarity 100.
Matches 18; Conservative
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; probe; ss;
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide agrenation, comprising any of the 6888 amino acid sequences in the specification, or their complements or fragments, and endoding at least 8 amino acids of any of the 6888 amino acid sequences ("LII) defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule cypression (comprising a plurality of single exon nucleic acid molecule active above, where each of the plurality of probes for measuring human calls or tissues. Also included are a spatially.

CC exon microarray for measuring human gene expression, a method of maddressably isolatable or amplifiable from the plurality, a single contiguous amino acids of any of the above-mentioned amino acid econtiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid soft accordance destring and/or licensing single exon probes or microarrays to a customer destring to measure gene expression, a method of providing soft accordance destring and/or licensing single exon probes or microarrays.

CC active above. The probes may be used as tools for surveying troage medium which contains a database having a plurality of records crited above. The probes may be used as tools for surveying a trasuse to detect the presence of expression of a single exon probe crited above. The probes may be used as tools for surveying alternation single exon, or in constructing genome-derived single exon microarrays.

CC in addition, the probes are used in identifying and characterising alternations in the genomic locument and
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100.0%; Score 18; DB 12; Length 587; 100.0%; Pred. No. 28; Sequence 587 BP; 130 A; 193 C; 129 G; 135 T; 0 U; 0 Other; 100.08; Best Local Similarity Query Match

AAH48169 standard; DNA; 636 BP (first entry) 21-SEP-2001 AAH48169;

Mutant bcl-XL coding sequence.

antidiabetic; apoptosis inhibitor; cellular uptake; anti-apoptosis; ischaemic disease; myocardial infarct; AIDS; neurodegenerative diseases; infective multiple failure; fulminant hepatitis; diabetes; mutant; domain; cardiant; anti-HIV; neuroprotective; hepatotropic; Bcl-2;

sapiens Synthetic. HOMO

WO200148014-A1.

05-JUL-2001

26-DEC-2000; 2000WO-JP009274 99JP-00371449

27-DEC-1999;

(SHIO) SHIONOGI & CO LTD

Tsujimoto Y; Shimizu S,

WPI; 2001-418246/44. P-PSDB; AAG64285.

BH4-fused polypeptides with peptide sequences capable of exerting effect on enabling uptake into cells, applicable as effective apoptosis inhibitors, useful in preventives or remedies for ischemic diseases e.g. myocardial infarct.

Disclosure; Page 66-68; 84pp; Japanese

The present invention relates to BH4-fused polypeptides. The BH4-fused polypeptide have a sequence capable of affecting cellular uptake and also as BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The BH4-fused polypeptides are useful as effective apoptosis inhibitors, and are useful in preventives or remedies for ischaemic diseases e.g. myocardial infarct, AIDS, neurodegenerative diseases, infective multiple failure, fulminant hepatitis and diabetes. The present sequence is a mutant bcl-XL sequence which was used in the present invention. This sequence was derived from a human bcl-XL DNA sequence

Sequence 636 BP; 148 A; 158 C; 207 G; 123 T; 0 U; 0 Other;

ö 100.0%; Score 18; DB 4; Length 636; 100.0%; Pred. No. 28; 0; Indels 0; Mismatches 100.08; Local Similarity 100.0 nes 18; Conservative Query Match Matches

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Gaps

AGTTCCACAAAAGTATCC 501 1 AGTICCACAAAAGIAICC 18

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AAH43464/c

AAH43464 standard; cDNA; 702 BP 04-DEC-2001 (first entry) AAH43464;

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Gaps

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0; Indels

Mismatches

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18; Conservative

Matches

ò 염

CDNA clone HP03564 ORF.

Npw38; NpwBP; protein interaction; reporter function; eukaryotic cell; localization; protein network; intracellular; primer; amplify; PCR; polymerase chain reaction; mitochondria; ss.

Homo sapiens

WO200168885-A1.

20-SEP-2001.

13-MAR-2001; 2001WO-JP001973

15-MAR-2000; 2000JP-00073095. 24-AUG-2000; 2000JP-00254418

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

Otake M; Nagata N, Eguchi C, Kato S,

WPI; 2001-590069/66. P-PSDB; AAB47515 Detection of protein-protein interactions for screening compounds capable of modifying the interaction comprises observing intracellular localization of one protein after altering the modification pattern.

Example 6; Page 27-29; 33pp; Japanese

X8888888888888

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This sequence represents the open reading frame of the mitochondrial cDNA clone HP03564. The protein encoded by this sequence was used in the method of the invention. The method allows detection of interactions between a protein X and a protein Y which has a reporter function in eukaryotic cells, and comprises modifying the localization patterns of X and/or Y, and the localization of Y in the cell is observed using the reporter function. This method is useful for the elucidation of protein networks within the cell. It is also applicable for the discovery of new proteins and low-molecular drugs, by observing their effect on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intracellular protein interactions
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Sequence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 U; 0 Other;

ö Gaps . 0 Query Match 100.0%; Score 18; DB 5; Length 702; Best Local Similarity 100.0%; Pred. No. 29; Matches 18; Conservative 0; Mismatches 0; Indels

ð g

ADM45994 standard; cDNA; 702 BP RESULT 15 ADM45994/c

ADM45994;

(first entry)

03-JUN-2004

random oligonucleotide library; protein interaction; ligand; receptor binding site; ss; gene; human; apoptosis inhibitory factor; Human apoptosis inhibitory factor Bcl-xL cDNA.

Homo sapiens

/*tag= a /product= "Human apoptosis inhibitory factor Bcl-xL protein" Location/Qualifiers 1. .702

JP2004024078-A.

29-JAN-2004

24-JUN-2002; 2002JP-00183456

24-JUN-2002; 2002JP-00183456

(SERE-) SERESUTA REKISHIKO SCI

Ä.

WPI; 2004-161478/16. P-PSDB; ADM45995.

Random oligonucleotide useful for detecting protein interaction, having base sequence, where each base of 1st and 2nd of the codon is the any of G, C,T (U), or A and the base of 3rd of codon is G or G, or G or T (U). Example 2; SEQ ID NO 3; 43pp; Japanese.

The invention relates to a novel random oligonucleotide having a base sequence where each base of the 1st and 2nd codon is any of ${\bf G}$, ${\bf C}$ T $({\bf U})$ or A and each base of the 3rd codon is ${\bf G}$ or C or T $({\bf U})$. The methods of the invention may be useful for preparing a random oligonucleotide preparation to be used for detecting protein interactions or for screening ligand or receptor protein binding sites. The current sequence is that of the human apoptosis inhibitory factor BCl-xL cDNA of the

Gaps ö 100.0%; Score 18; DB 12; Length 702; 100.0%; Pred. No. 29; Seguence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 U; 0 Other; 0; Indels Mismatches . 0 18; Conservative Local Similarity Query Match Best Local S Matches 18 S

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1 AGTICCACAAAAGIAICC 18

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581 AGTICCACAAAAGTAICC 564

Search completed: February 4, 2005, 21:52:43 Job time: 232.23 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on:	Indian	Pred. No. is the number of results predicted by chance to hav score greater than or equal to the score of the result being and is derived by analysis of the total score distribution. SUMMARIES sult No. Score Match Length DB ID 1 18 100.0 167 2 BF929309 1 18 100.0 231 4 BM818607 BF806802	C 5 18 100.0 256 4 BM044697 BM044697 6 BM044697 6 AM23588 BM044697 CON 60 10 10 10 10 10 10 10 10 10 10 10 10 10

CF147016 UI-HF-CB0	BE293685 60118694	BI252492 60295295	BI457116 60318536		BG290422 60238827	BG470667 60251159	CD636470 56049223	CD636468 56049107	BG748447 602706419	BF569393 60218565	BE512918 60117214	BE249973 60094314	BQ687097 AGENCOUR	BU528551 AGENCOUR	CK000319 AGENCOUR	BI222971 60294346;	BQ943707 AGENCOUR	CF619432 AGENCOUR		BO962018 AGENCOUR
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1 (bases 1 to 216)

1 (bases 1 to 216)

1 (bases 2 to 216)

1 (bases 3 to 216)

Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., G. Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                   BF806802 216 bp mRNA linear BST 12-JAN-2001
PM2-C10111-091100-004-b10 C10111 Homo sapiens cDNA, mRNA sequence.
BF806802
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Fax: +55-11-2707001

Fax: +55-11-2707001

Fax: +55-11-2707001

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Fax: +55-11-2707001

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMZ£t2=PMZ-CI0111-091100-004-bb.0£t3=2000-11-09£t4=1)

Seq primer: puc 18 forward

High quality sequence start: 25

High quality sequence start: 25

High quality sequence stop: 216.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
                                                                                                                                        100.0%; Score 18; DB 2; Length 167; 100.0%; Pred. No. 1.7e+02;
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/organism="Homo sapiens"
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EST 06-MAR-2002 K-EST0085942 S20T665307 Homo sapiens CDNA clone S20T665307-4-B02 5/, MENA sequence.
                                                                                                                                                                                           1 (bases 1 to 231)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF804861 232 bp mRNA linear EST 12-JAN-2001
PM2-CI0111-041100-001-d01 CI0111 Homo sapiens CDNA, mRNA sequence.
BF804861
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Korea Research Institute of Bioscience & Biotechnology
Secondomy Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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100.0%; Pred. No. 1.8e+02;
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21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 231
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/clone="S20T665307-4-B02"
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Plate: 4 row: B column: 02
High quality sequence stop: 231.
Location/Qualifiers
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                                                                                                                        Homo sapiens (human)
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Contact: Kim YS
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Matches 18; Conserv
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Query Match 100.0%; Score 18; DB 2; Length 216; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 18; Conservative 0; Mismatches 0; Indels

MEDLINE PUBMED

COMMENT

JOURNAL

TITLE

REFERENCE AUTHORS

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/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into BcoRI/AhoI sites using the following 5' adaptor: GGGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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maall: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1938 row: c column: 02
High quality sequence stop: 171.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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           Unpublished (1999)
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/mol Lype="mrm" diptom.
/db xref="taxon:9606"
/db xref="taxon:9606"
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/clone lib="Clone" diptom.
/mote="Corgan: colon ins; Vector: puc18; Site 1: Smal;
Site 2: Smal; A min1-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                 Dias Neto, E., Carcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pax: +55-11-2707001
Mahall: adimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?t1=PM2&t2=PM2-CI0111-04100-001-401&t3=2000-11-04&t4=1)
Seq primer: puc 18 forward
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
baboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 232.
Location/Qualifiers
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        GI:12133850
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                                                         sapiens (human)
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                                                                                                                                                                   (bases 1 to 232)
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BM049697
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FEATURES

RESULT 5 BM049697/c DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE

EST 13-JAN-2001 mRNA sequence.

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AW820530/c
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                                                                                                                                                            /mol_type="mRNA"
/db xref="texon:9606"
/db xref="texon:9606"
/dev_stage="Adult"
/clone_lib="RT0055"
/note="forgan: Ridney tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Far. +55-11-2707001

Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-140
200-042-f12&t3=2000-02-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 332.
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QV2-ST0298-140200-042-f12 ST0298 Homo sapiens CDNA, mRNA sequence.
AW820481
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1 (bases 1 to 33)

1 (bases 1 to 32)

2 (bases 1 to 32)

3 (bases 1 to 32)

3 (bases 1 to 32)

4 (bases 1 to 32)

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(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-
221200-011-G02&t8=122000-12-22&t4=1)
Seg primer: puc 18 forward
High quality sequence stop: 283.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/clone_lib="ST0298"
                                                                                                                                           /organism="Homo sapiens"
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Location/Qualifiers
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AW820481/c
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AUTHORS
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Eukaryoffa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-220
200-061-d10&t3=2000-02-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 358.
Location/Qualifiers
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Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Indwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
/note="Organ: stomach; Vector: puc18; Site 1: Smal; Stal; Stal 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=cW3&t2=CM3-GN0297-110101-607-f03&t3=2001-01-11&t4=1) Seq primer: puc 18 forward High quality sequence start: 3 High quality sequence start: 3 High quality sequence stop: 418.
       BI051278 418 bp mRNA linear EST 15-JUN-2001
CM3-GN0297-110101-607-£03 GN0297 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: placenta_normal, Vector: puc18, Site_1:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcribtion of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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K-EST0014589 S6SNU620 Homo sapiens CDNA Clone S6SNU620-4-C01 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 1.9e+02;
    mRNA
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone_lib="GN0297"
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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                                                                         BI051278.1 GI:14458808
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/clone_lib="S207665307"
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Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (RAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
inteat mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by.
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 6 font. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
                                                                                                                                                                                                        396 bp mRNA linear EST 06-MAR-2002
K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03
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Kim,N.Ş., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Conteact: Kim Yes.

Genome Research Center

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Email: yongsung@mail.kribb.re.kr

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High quality sequence stop: 396.
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    100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0;
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Kim, Y.S.
21C Frontier Korean EST Project 2001
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FEATURES

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RESULT 9 BM818649/c DEFINITION

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Gaps . EST 01-MAR-2002

Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

RESULT 10 BIO51278

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                   Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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Ok64a12.si NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518718 3'
similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X.;, mRNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 442)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                           Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
72: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
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High quality sequence stop: 418.
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                                                                                         21C Frontier Korean EST Project 2001
Unpublished (2002)
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

cDN Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-blo.llhi.gov/bprp/image/image.html

Insert Length: 536 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type==projed germ cell tumors"
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polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTyT3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo.
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1 (bases 1 to ...)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Rin, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)
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Korea Research Institute of Bioscience & Biotechnology
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongeungemail.kribb.re.kr
Plate: 3 row: B column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 18; DB 1; Length 442; 100.0%; Pred. No. 2e+02;
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High quality sequence stop: 447.
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ORIGIN

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/GDL type="mRNA"
// Ab xref="taxon:9606"
/ Clone="INARA"
/ Lissue_Type="endometrium, adenocarcinoma cell line"
/ Lissue_type="endometrium, adenocarcinoma cell line"
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM263 row: b column: 07
High quality sequence start: 4
High quality sequence stop: 479.
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
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Site 2: Smal; A mini-library was made by cloning products
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No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                              AWB14883 17-MAY-2000 MRNA linear EST 17-MAY-2000 MR1-ST0206-120400-022-£04 ST0206 Homo sapiens cDNA, mRNA sequence. AW814883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 486)
Dias Neto, E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR1-ST0206-120 400-022-f04&t3=2000-04-12&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                              Gaps
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Pred. No. 2e+02;
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High quality sequence stop: 485
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100.0%;
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                                                           Conservative
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Matches 18; Conserv
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Search completed: February 5, 2005, 08:11:52 Job time : 2147.2 secs

Scoring table:

Searched:

Sequence:

Title:

OM nucleic

Run on:

08 08

Minimum I Maximum I

Database

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BT008248 Synthetic
AR05402 Sequence
AR172595 Sequence
152012 Sequence
7837166 Sequence
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AR12495 Sequence
AR144311 Sequence
AR172594 Sequence
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AR172594 Sequence
AR172594 Sequence
BD243042 Antisense
CQ765842 Sequence
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                                                                                                                                                                                                                                     AR371661 Sequence
AR380885 Sequence
AX839772 Sequence
AX925686 Sequence
Z23115 H.sapiens b
AX085490 Sequence
BD102202 Method of
BD102202 Method fo
BT107208 Homo sapi
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PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1998 US 09/109614
PI CY A STEIN
PC
C12N15/09.A61K9/127,A61K9/51,A61K31/711,A61K31/7125, 1
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Patent: JP 2002s19048-A 12 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/12
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 18 bp DN of bcl-xL.
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            BD102202
BT007208
BT008248
AR054022
AR172595
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AR380913
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AR054021
AR118504
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CQ138771 Sequence
CQ25995 Sequence
CQ25995 Sequence
CQ2734058 Sequence
                                                                             ; Search time 432.664 Seconds (without alignments)
1967.381 Million cell updates/sec
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           GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                               4526729 seqs, 23644849745 residues
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CQ732731
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PAT 17-JUL-2003
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Datent: JP 2002519048-A 33 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
N Artificial Sequence
N JP 2002519048-A/33
PD 02-JUL-2002
PF 02-JUL-1999 JP 2000557839
PR 02-JUL-1999 US 09/109614
PI CY A STEIN
PC CLINIS/09,A61K9/127,A61K9/51,A61K31/711,A61K31/7125, PC
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/mol_exee="taxon:9606"
/note="MAP TO AL117381.9~EXPRESSED IN PLACENTA, SIGNAL =
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
Patent: WO 01527272-A 21529 09-AUG-2001;
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PC A61K47/42,
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
FH Key
FT misc binding (1) . (4)
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_kref="taxon:32630"
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Patent: JP 2002519048-A 32 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
Artificial Sequence
N JP 2002519048-A/32
PD 02-JUL-1999 JP 2000557839
PR 02-JUL-1999 US 09/109614
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/mol_type="genomic DNA"
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Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
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/db xref="texon:9606"
/note="MAP TO ALL1731.9-EXPRESSED IN BONE MARROW, SIGNAL
- 5.5-WISSPROT HIT: QO7817, EVALUE 2.00e-16-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
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1.5-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE 1.00e-65"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
Patent: WO 015/2276-A 21565 09-AUG-2001;
Acomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
Patent: WO 015/274-A 16681 09-AUG-2001;
Aeomica, Inc. (US)
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CQ151543
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Sequence 16681 from Patent WO0157274.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    127
    organism="Homo sapiens"

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Location/Qualifiers
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= 1.9-SWISSPROT HIT: Q07817, EVALUE 2.00e-18-EST_HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER-130- PB 0004 WO 3<br/>
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150-00 US 60/1805,312-151- 04 February 2000 (04.02.00)<br/>
60/207,456-151- 26 May 2000 (26.05.00)<br/>
60/207,456-151- 26 May 2000 (26.05.00)<br/>
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 20737 from Patent WO0157277.
CQ272476
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SIGNAL = HUMAN HIT:

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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                            Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain
Patent: WO 0157275-A 20846 09-AUG-2001;
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                                                                                                                                                                       /mol_type="unassigned DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0;
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PE Corporation (NY) (US)
Location/Qualifiers
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CQ099589.1 GI:41068615
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/db_xref="taxon:9606"
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                                                                                              Aeomica, Inc. (US)
Location/Qualifiers
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Matches 18; Conservative
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Matches 18; Conservative
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= 4.1-SWISSPROT HT: Q07817, EVALUE 2.00e-10-EST HUMAN

HT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
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/organism="Homo sapiens"
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/db xref="texcn:9606"
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1.00e-65"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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analysis of gene expression in human fetal liver
Patent: WO 0157277-A 20737 09-AUG-2001;
Aeomica, Inc. (US)
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Human genome-derived single exon nucleic acid analysis of gene expression in human lung
Perent: WO 0186003-A 21250 15-NOV-2001;
Aeomica, Inc. (US)
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Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
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Seguence 21250 from Patent WO0186003.
CQ310145
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Sequence 20846 from Patent WO0157275.
CQ346752.
CQ346752.1 GI:41295823
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/organism="Homo
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= 5.5"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                 1. 587
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 8597 09-AUG-2001;
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Human genome-defived single exon nucleic acid probes useful for
analysis of gene expression in human heart
Patent: WO 0157274-A 6802 09-AUG-2001;
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0;
Patent: WO 0157272-A 8448 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Location/Qualifiers
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3-L150- US 60/180, 312-1151- 04 February 2000 (04.02.00)<br/>
60/207,456<151- 26 May 2000 (26.05.00)<br/>
60/207,456<151- 26 May 2000 (26.05.00)<br/>
60/207,456<151- 26 May 2000 (26.05.00)<br/>
60/207,09.00<br/>
60/200 (03.08.00)<br/>

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100.0%; Pred. No. 1.8e+02;
Mismatches 0;
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/organism="Homo sapiens"
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CQ221990.1 GI:41204114
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- nucleic search, using sw model OM nucleic

February 4, 2005, 15:50:53 Run on:

; Search time 232.23 Seconds (without alignments) 406.880 Million cell updates/sec

US-09-753-169A-12 18

Title: Perfect score:

1 ctttcggctctcggctgc 18 Sequence: .

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4134886 segs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04:* Database :

geneseqn2003cs: geneseqn2003ds: geneseqn2001as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2001bs:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2002as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

		Description	Aaz46982 Bcl-X1 mR	Adp17303 Renal cel	Adg89109 Cancer de	Adp27571 Human Bcl	Aba72432 Human foe	Aai52843 Probe #21	Aba38215 Probe #16	Aak47008 Human bon	Aak20855 Human bra	Abs46769 Human liv	Abs21259 Human gen	Ach84269 Human gen	Acd94503 Human col	Adk66037 Standardi	Ach46093 Human inf	Human	Aai39762 Probe #84	Aba28336 Probe #68	Aak34040 Human bon	Aak08161 Human bra	Abs33839 Human liv
SUMMARIES	;	at .	AAZ46982	ADP17303	ADG89109	ADP27571	ABA72432	AA152843	ABA38215	AAK47008	AAK20855	ABS46769	ABS21259	ACH84269	ACD94503	ADK66037	ACH46093	ABA59891	AAI39762	ABA28336	AAK34040	AAK08161	ABS33839
	í	BO !	٣	12	10	12	4	4	4	4	4	4	9	12	10	10	6	4	4	4	4	4	4
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de	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100,0	100.0	100.0	100.0	100.0	100.0	100.0
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1000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		ABS08825	ACH70569	AAH48169	AAH43464	ADM45994	AAQ81699	ABZ83507	ADI32132	ADG65218	AAF30926	ADG65209	AAQ81698	AAT40079	AAZ93614	AAS15189	AAC90810	ABK84766	ABT16641	ADD56779	AAD64187	ADI32104	ADH52630	AD019990	ADP13351
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2 2 2 2 3 3 3 3 3 3 3 3 4 4 4 4 1 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 8 1 1 8 1 1 8 1		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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		22	c 23	c 24	c 25	c 26	c 27	c 28	c 29	c 30	c 31	c 32	c 33	c 34	c 35	c. 36	c 37	c 38	c 39	c 40	c 41	c 42	c 43	c 44	c 45

ALIGNMENTS

Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Bcl-X1 mRNA specific antisense oligo L. AAZ46982 standard; DNA; 18 BP 14-APR-2000 (first entry) WO200001393-A2. Homo sapiens. AAZ46982; RESULT 1 AAZ46982

13-JAN-2000.

99WO-US015250. 02-JUL-1999; 98US-00109614. 02-JUL-1998; (UYCO) UNIV COLUMBIA NEW YORK.

Stein CA;

WPI; 2000-137140/12.

New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

The invention provides antisense oligonucleotides or their derivatives which reduce or eliminate expression of the anti-apoptotic protein belact. The oligonucleotides can be introduced into tumour cells to reduce belact production to treat cancer. Oligonucleotides comprising one or more prostate, lung or bladder cancer. Oligonucleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bol. Z family proteins (to which belack belongs) in such treatment. The oligonucleotides can be introduced into vascular cells to reduce belaction to promote the regression of vascular

RCC and/or other solid tumors. This sequence corresponds to a probe to detect a gene that is differentially expressed and detected by the method of the invention.

Seguence 25 BP; 8 A; 6 C; 10 G; 1 T; 0 U; 0 Other;

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Gaps

. 0

Indels

Score 18; DB 12; Length Pred. No. 25; Mismatches 0; Indels

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100.0%;

Query Match 100. Best Local Similarity 100. Matches 18; Conservative

1 CTTTCGGCTCTCGGCTGC 18

CTTTCGGCTCTCGGCTGC 6

23

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25;

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lesions. They can also be included with a carrier (and optionally tetra asso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-XI mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in paripheral blood samples isolated at different stages of progression, development or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renal cell carcinoma differentially expressed gene probe #3708
                                                                                                                                                                                                                      100.0%; Score 18; DB 3; Length 18; 100.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                            Sequence 18 BP; 0 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                        0; Mismatches
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2003US-0459782P.
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                                                                                                                                                                                                                                                                                                                                                                                      1 CTTTCGGCTCTCGGCTGC
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ADP17303 standard; DNA; 25
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                                                                                                                                                                                                                                                                                    18; Conservative
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BURCZYNSKI M E.
TREPICCHIO W L.
DORNER A.
STOVER J A.
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                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP17303;
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                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STOV/)
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                                                                                                                                                                                                                                                                                        Matches
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ADP17303/

MXX
ADP17303/
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The invention relates to a method of predicting clinical outcome for a patient diagnosed with cancer by determining the expression level of or or more genes, or their expression products, selected from p53BP2, cathepsin L, Ki67/MiB1, and thymidine kinase in a cancer tissue obtained from the patient, normalized against control gene(s), and compared to the amount found in a reference cancer tissue set. The specification also discloses an array comprising polynucleotides hybridizing to the following genes: FOXMI, PRAME, Bcl2, STKIS, CEGP1, Ki-S7, GST, GTM1, CA9, PR, BBC3, NME1, SURV, GAT3, TPRC, CAB2, CDC25B, IGFTR, AK055699, P13KC2A, TGFB3, BAG11, CYP3A4, EpCAM, VEGC, pS2, HENT1, WISP1, HNF3A, NFREMSES, BRCA2, EGRR, TKL, VDR, CORHISTON, DEATT, EPHRIT, IPTA, CDH1, HIFL, IGFBP3, CTSB, HAZ and D18ELO, immobilized on a solid surface. The methods are useful for predicting clinical outcome for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicting clinical outcome for a patient diagnosed with cancer comprises determining the expression level of one or more genes, and compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patient diagnosed with cancer, classifying cancer, and predicting the likelihood of Long-term survival of a breast cancer patient, or a patient diagnosed with invasive breast cancer or with estrogen receptor (ER) positive invasive breast cancer. This sequence corresponds to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Walker MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 70 BP; 19 A; 18 C; 21 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligonuclectide used in the method of the invention.
                                                                                                                                                          Cancer detection method related oligonucleotide #57
                                                                                                                                                                                                               estrogen receptor-positive invasive breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the amount found in a reference cancer tissue set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shak S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 57; 198pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kiefer MC,
                                      ADG89109 standard; DNA; 70 BP
                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2003; 2003WO-US007713.
                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2002; 2002US-0364890P.
18-SEP-2002; 2002US-0412049P.
                                                                                                                                                                                                 ss; cancer; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) GENOMIC HEALTH INC.
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cronin MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-767536/72.
                                                                                                                                                                                                                                                                                               WO2003078662-A1.
                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                  11-MAR-2004
                                                                                                                                                                                                                                                                                                                                      25-SEP-2003.
                                                                             ADG89109;
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                  ADG89109,
RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressing head or neck cancer or colon cancer exhibits elevated or the decreased expression levels of these genes compared to normal. As such, these methods are also useful for prognosing or predicting the likelihood of cancer-attributable death or progression, including recurrence and entestatic spread of a neoplastic disease, as well as drug resistance. This polynucleoride sequence is a human PCR amplicon DNA sequence used as a prognostic cancer marker, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prognosing a patient with EGFR-expressing colon cancer comprises subjecting a sample comprising EGFR-expressing cancer cells to quantitative analysis of the expression level of the RNA transcript of at
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                      PCR amplicon; ds; prognostic marker; EGFR; cowth factor receptor; cancer; gene expression profilin head and neck cancer; colon cancer; metastatic spread;
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                DB 10; Length 70; 27;
                                                    Indels
                                                                                                                                                                                                                                                                                                                          Human Bclx DNA used as a cancer prognostic marker SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 70 BP; 19 A; 18 C; 21 G; 12 T; 0 U; 0 Other;
                                                    ö
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baselga J;
                Score 18;
Pred. No.
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100.0%; Scc.
100.0%; Pre
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                                                                                       18
                                                                                                          CTTTCGGCTCTCGGCTGC 30
                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one gene e.g., CD44v3.
                                                                                      1 CTTTCGGCTCTCGGCTGC
                                                                                                                                                                                                               ADP27571 standard; DNA; 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOMIC HEALTH INC
                                                                                                                                                                                                                                                                                    (first entry)
                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-420643/39.
                                                                                                                                                                                                                                                                                                                                                                                                                  neoplastic disease.
             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                              epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004046386-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                      26-AUG-2004
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                                                                                                                                                                                                                                                   ADP27571;
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                                                                                                                                                                                                ADP27571/c
                                                                                                                                                                              RESULT
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The
                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                             Human foetal liver single exon nucleic acid probe #20737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR
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2000US-0236359P.
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                                                                          ABA72432 standard; DNA; 127
                                                                                                                                   01-FEB-2002 (first entry)
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Matches 18; Conservative
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30-JUN-2000;
03-AUG-2000;
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Best Local Similarity 100. Matches 18; Conservative

Query Match

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WPI; 2001-488900/53
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                                                      Penn SG,
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                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #16681 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                     Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 21529; 654pp; English
                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                           gene expression in human placenta.
                                                                                                 04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-023455P.

04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
33-AUG-2000; 2000US-00632366.
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                                                                                 30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
         genetic disorder; ss.
                                                                                                                                                                                             Penn SG, Hanzel DK,
                                                                                                                                                                                                               WPI; 2001-488897/53
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                                             WO200157272-A2
                           Homo sapiens
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 16681; 530pp; English.
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                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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21-SBP-2000; 2000US-0234687P.
-ZBP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408.
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                                                                                                                            probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                                                                                          present invention provides a number of single exon nucleic acid
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                                                            Example 4; SEQ ID NO 21565; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                              Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
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                       gene expression in human bone marrow
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Best Local Similarity
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the

Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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                                           Gaps
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                                                                                                                                                                                                                                                                                   Human; single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
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                                           Indels
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                                                                                                                                                                                                                                                               Human liver single exon probe, SEQ ID No 21759.
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               Score 18; DB
Pred. No. 28;
                                         Mismatches
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Pred. No.
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100.0%; SCU.
100.0%; Pre
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                                                                                                                                                                         ABS46769 standard; DNA; 127 BP.
                                                                     1 CTTTCGGCTCTCGGCTGC 18
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2000US-0234687P.
2000US-0236359P.
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Best Local Similarity 100.0
Matches 18; Conservative
                                         Conservative
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         Query Match
Best Local Similarity
Matches 18; Conserv
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ABS21259 standard; DNA; 127 ABS21259; RESULT 11 ABS21259

BP.

(first entry) 19-AUG-2002

Human genome-derived single exon probe ORF from lung SEQ ID No 21250.

Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicorytosis; lymphangioleteiomyontosis; Karagener syndrome; pulmonary alveolar proteinnosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; single exon probe; asthma; lung cancer; COPD; ILD; hyaline membrane disease; open reading frame; ORF. Human; ds;

Homo sapiens

WO200186003-A2

15-NOV-2001

30-JAN-2001; 2001WO-US000665

2000US-0207456P 2000US-00608408 2000US-0180312P 04-FEB-2000; 26-MAY-2000;

03-AUG-2000; 21-SEP-2000; 27-SEP-2000;

; 2000US-00632366. ; 2000US-0234687P. ; 2000US-0236359P. ; 2000GB-00024263. 04-OCT-2000;

(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR; Penn SG, Hanzel DK,

WPI; 2002-114183/15

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 4; SEQ ID NO 21250; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes with the human lung, reading frames derived from the 12614 probes with the human lung, comprising expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably can be also array and a least one exon from genomic sequences of the abeled mucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon; the probe is included in the above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon discrearrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that

the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-histiocytosis, lymphangioleiomyomtosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary dysplasia, primary ciliary karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary cyclesent sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 888888888888888888888

Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;

Gaps . 0 6; Length 127; 0; Indels Score 18; DB Pred. No. 28; Mismatches .. 100.0%; Query Match 100. Best Local Similarity 100. Matches 18, Conservative

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4CH84269/

ACH84269 standard; DNA; 179

ACH84269;

29-JUL-2004

(first entry)

Human genome derived single exon probe #17464.

Human, probe, ss, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386.

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Hanzel DK; Rank DR, Penn SG,

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 1; SEQ ID NO 17464; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-

WPI; 2003-182626/18.

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                                                                                                                                                                                                                                                                                                                                                                                                                                             alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                        methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Open reading frame detection; genome sequencing; colon cancer; breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovinus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above,
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Mismatches
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Best Local Similarity 100.
Matches 18; Conservative
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Brentani RR;

Neto ED,

AJG,

(SIMP/) SIMPSON A J G. BRENTANI R R. NETO E D.

(NETO/) (BREN/) Simpson

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the genome of organism. Comprising contectmining Open reading I range I net genome of organism comprising contecting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing single estranded cDNA by reverse transcribing mRNA with (I), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting and amplifying steps with different primers and sequencing resulting and entered is useful for: determining that a known nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a contig, nucleotide sequence of an open reading frame; for preparing a contig, and lor part of a genome of an organism. mRNA is obtained from mammalian correlation correct cell rife method is useful for analyses of copulations of subjects and can be used to carry out genetic analyses of populations of subjects and can be used to study living systems to determine if, e.g. there have been selected to study living systems to determine if, e.g. there have been selected with diseases such as cancer, to determine antibiotic resistance or nondividual or population more or less likely to be afflicted with diseases such as cancer, to determine antibiotic resistance or nondiseases such as cancer, to determine antibiotic resistance or nondiseases such as cancer, to determine antibiotic resistance or nondiseases such as cancer, to determine antibiotic resistance or nondiseases such as cancer, to determine antibiotic resistance or nondiseases such as cancer, to determine if estimates for a selection or a footus, as well as the study of whether the conditions are likely to be passed to offspring threaded to determine; plants, birds, lish, etc. Using this method, in all animals, plants, birds, lish, etc. Using this determine if resistance genes are present, defects in plant genomes can also be studied in this way, similarly, the method essentially plants of the rapt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library
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functional genomics; sample analysis; pharmacogenomics; sample analysis.
                                     Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of individual.
                                                                                                                                                                                                          The invention describes a method of determining open reading frames in
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Pred. No. 29;
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                                                                                                                                                           Example 9; Page 432; 959pp; English.
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Best Local Similarity
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Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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tes 18; Conservative (
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STACHE-CRAIN
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                                                                                                                                                               Koehler T,
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(first entry)

Mismatches

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Jones LW;

Stache-Crain B, Dickson MC,

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/SST sequences. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                          New polynuclectide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtained in electronic format directly from USPTO seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                       Claim 1; SEQ ID NO 33305; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
       The present invention relates to a standardized polynucleotide system, which comprises at least one carrier nucleic acid, at least 3 bigonucleotides, as primers and target-specific, fluorescently labeled probe and optionally at least one set of stabilized controls (standard RNA or DNA) of known concentration and instructions. The system comprises any of 20 sets of one control, two primers and one target-specific probe. The standardized polynucleotide system can be used for quantitative, real-time detection of target nucleic acids, especially analysis of genes or gene products, e.g. for individualized medical diagnosis, in veterinary medicine, functional genomics, clinical pharmacology, pharmacogenetics, pharmacocle and lesting, analysis of food or environmental samples and also for ultra-sensitive detection of proteins by immuno-PCR. The present
                                                                                                                                                                                                                                                                                                                                                               Standardized polynucleotide system, useful for quantitative, real-time determination of nucleic acid, comprises stabilized standards, primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is a polynucleotide used in the system of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;
                                                                                                                                               (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 7; 38pp; German.
28-FEB-2002; 2002DE-01009071
                                                                       28-FEB-2002; 2002DE-01009071
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Gaps
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                              100.0%; Score 18; DB 9; Length 492; 100.0%; Pred. No. 30; ive 0; Mismatches 0; Indels
Sequence 492 BP; 112 A; 117 C; 154 G; 109 T; 0 U; 0 Other;
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C 25 18 100.0 687 2 BE293685 BE293685 BE293685 BE352492 60252857 C 27 18 100.0 695 4 BI252492 BE370269 601447403 C 28 18 100.0 700 4 BG301301 BC380120 BC380120 BC370422 60252857 C 29 18 100.0 700 4 BG470667 BC370422 BC370422 602308270 C 29 18 100.0 714 4 BG470667 BC470667 GC5211594 C 30 18 100.0 726 CD63468 BC470667 GC5211594 C 31 18 100.0 728 4 BG470679 BC634107 GC6536468 BC6341070 GC6536468 BC6341070 GC6536468 BC636468 BC626491070 GC6536468 BC636468 BC636468 BC636468 BC636468 BC636468 BC636468 BC636468 BC636468	RESULT 1 BF929309 167 bp mRNA linear EST 19-JAN-2001 DEFINITION IL2-NT0202-081200-298-DD5 NT0202 Homo sapiens cDNA, mRNA sequence. ACCESSION BF929309 16.12327437 ACCESSION BF929309.1 GI:12327437 REPERSION BF929309.1 GI:12327437 SOURCE BAT. ORGANISM Homo sapiens (human) AURINORD Sapiens (human) Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (Dases I to 167) AUTHORS Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A. Barda,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Matcher,P.S., Jongeneel,C.V., Shorgan,A., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags JONDRAD PROSE Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	PUBMED 10737800 COMMENT Conteact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=ILi2&t2=ILi2-NT0202- 081200-228-D05&t3=2000-12-08&t4=1) Seq primer: puc 18 forward High quality sequence stop: 167. Seq primer: puc 18 forward High quality sequence stop: 167. FEATURES Location/Qualifiers
Copyr - nucleic se Pebruaz US-09-7 ore: 18 1 cttc ole: IDENTIT 3282287 er of hits sa	Maximum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 100% Listing first 45 summaries Database : EST:* I gb_estl:* 2: gb_estl:* 3: gb_htc:* 3: gb_htc:* 4: gb_estl:* 5: gb_estl:* 5: gb_estl:* 5: gb_estl:* 5: gb_estl:* 6: gb_estl:* 6: gb_estl:* 6: gb_estl:* 7: gb_estl:* 8: gb_gssl:* 8: gb_gssl:* 9: gb_gssl:* 8: gb_gssl:* 9: gb_gssl:* 8: gb_gssl:* 9: gb_gssl:* 8: gb_gssl:* 9: gb_gssl:*	c 1 18 100.0 167 2 BF9029309 BF9029309 ILC-NTO20 3 18 100.0 232 2 BF8066802 BF804861 PM2-CI011 c 4 18 100.0 233 1 A1904167 AR80461 PM2-CI011 c 4 18 100.0 233 2 AM820481 QV2-CI011 c 6 18 100.0 233 2 AM820481 QV2-CI014 c 7 18 100.0 339 2 BR925384 BR920538 RCS-RT005 c 9 18 100.0 336 4 BM182649 RCS-RT005 c 9 18 100.0 356 4 BM182630 BM820534 BM820534 BM820534 BM820534 BM820534 BM820534 BM820536 CCS-RT0014 c 13 10 418 4 BM18387 BM320334 BM320334 BM320334 CCS-CT0

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1 (bases 1 to 216)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman, M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Go'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-
091100-004-bl0&t1=2000-11-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 216.
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PM2-CI0111-091100-004-b10 CI0111 Homo sapiens CDNA, mRNA sequence.
BF806802
No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                   DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                              100.0%; Score 18; DB 2; I 100.0%; Pred. No. 2.4e+02;
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Homo sapiens
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Matches 18; Conservative
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/mol_type="maxma" suprems /mol_type="maxma" suprems /mol_type="maxma" suprems /mol_type="maxma" suprems /db xref="taxon:9606" /db xref="taxon:9606" /clone lib="taxon:9606" /clone lib="taxon: colon ins; Vector: puc18; Site 1: Smal; Site 2: Smal; A min1-library was made by cloning products stee2 from ORSENTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) porfiles into the pUC18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 223)
1 (bases 1 to 223)
Dias Neto. Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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CM-BT043-090299-089 BT043 Homo sapiens cDNA, mRNA sequence.
A1904167
                                                                                                                                                     212 bp mRNA linear EST 12-JAN-2001
PM2-CI0111-041100-001-d01 CI0111 Homo sapiens CDNA, mRNA sequence.
BF804861
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Fax: +55-11-270001
Fax: +56-11-2707001
Fax: +56-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts//gethtml2.pl?tl=PMZ&t2=PMZ-CI0111-041100-001-d01&t3=2000-11-04&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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/organism="Homo sapiens"
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High quality sequence start: 13
High quality sequence stop: 232.
Location/Qualifiers
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                            112 CTTTCGGCTCTCGGCTGC 129
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1 CITICGGCICICGGCIGC 18
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Matches 18; Conserv
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                                                                                                                        RESULT 3
BF804861
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Gaps

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100.0%; Score 18; DB 2; Length 216; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels

Conservative

Local Similarity nes 18; Conserva

Matches

Query Match

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Tell +32-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-
221200-011-G02&t3=2000-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol Lype="mrm" diptum:
//mol Lype="mrm" diptum:
/db xref="taxon:9606"
/db xref="taxon:9606"
/dcome lib="Adult"
/clone lib="Ryc055"
/note="Organ: Kidney tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - budwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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(base 1 to 332)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordini,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW820481 332 bp mRNA linear EST 17-MAY-2000 QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonió Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                         expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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100.0%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
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Best Local Simi
Matches 18;
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                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 23)

1 (bases, M.R., Bordin, S., Briones, M.R., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., G. Harse, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="Adult"
/clone lib="BT043"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2:
Smal; A min:-library was made by cloning products derived
from ORESTES POR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the DUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpsoneoludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html
&t3=090299&t4=1)
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1 (Dases 1 to 283)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P.; Jongeneel,C.V.,
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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stringency conditions.
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Location/Qualifiers
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  AI904167.1 GI:6494554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
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/mol_Lype="mrm" orpromed for the factor of t
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 358)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, D.F., de Souza, S.J. and
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/clone lib="ST0298"
/note="Organ: stomach; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cToning products
derived from ORESTES PCR (U.S. Letters Patent application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This erry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-220
200-061-d10&t3=2000_02-22&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
                                                                 organism="Homo sapiens"
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High quality sequence start: 44
High quality sequence stop: 358
Location/Qualifiers
location/Qualifiers
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Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PMO-AN0087-180
Seq primer: puc 18 forward
                                                                                                                       This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-140 200-402-fl2&t3=2000-02-14&t4=1) Seq primer: puc 18 forward fligh quality sequence stop: 332.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Harr, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
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PMO-AN0087-180800-001-b07 AN0087 Homo sapiens CDNA,
BE925384
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Pred. No. 2.5e+02;
; Mismatches 0;
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/organism="Homo sapiens"
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High quality sequence stop: 339
                    Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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Mismatches
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/organism="Homo sapiens"
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High quality sequence start: 3
High quality sequence stop: 418.
Location/Qualifiers
                                            CITICGGCTCTCGGCTGC 232
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//done libe_s20T665307
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K-EST0085991 S20T665307 Homo sapiens cDNA clone S20T665307-4-F03
BM818649
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1 (bases 1 to 396)
1 (bases 1 to 400, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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competent cells E. coli ToptOF. by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fat: +82-42-860-4470
Fax: +82-42-860-4409
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/mol_type="mRNA"
/db xref="taxon:9606"
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Plate: 4 row: F column: 03
High quality sequence stop: 396.
Location/Qualifiers
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/mol_type="maxxx" corrections of the pure large and the pure large and
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Didases I to 418)
Dias Naco, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., Gouza, S.J. and Simpson, A.J.
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Fax: +55-11-270001
Fax: +56-11-2707001
Fax: +56-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.b/fscripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-10101-607-f03&t3=2001-01-11&t4=1)
HI051278 418 bp mRNA linear EST 15-JUN-2001
CM3-GN0297-110101-607-£03 GN0297 Homo sapiens CDNA, mRNA sequence.
BI051278
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/cell_type="Scattering floating"
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/cell_the="Scattering floating"
/lab_host="ToploF"
/lone_lib="ScSNU620"
/note="Organ: Stomach; Vector: pCNS; Site_l: EcoRI;
/note="Organ: Stomach; Vector: pCNS; Site_l: EcoRI;
/site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intext mRNA was ligated with DNA-RNA linker including EcoR is site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from obligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was
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                                                                                                                                                                            Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Far: +82-42-860-4470
Fax: +82-42-860-4409
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High quality sequence stop: 418.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="S6SNU620-4-C01"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 536 Std Error: 0.00
Seq primer: -40ml3 #wd. EF from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib= NGIC CGAP GC4"
/clone lib= NGIC CGAP GC4"
/clone lib= NGIC CGAP GC4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Patima Bonaldo. "
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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K-EST0085558 S20T665307 Homo sapiens cDNA clone S20T665307-3-B02
1 (bases 1 to 442)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Korea Research Institute of Bioscience & Biotechnology
$2 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongeungamail.kribb.re.kr
Plate: 3 row: B column: 02
High quality sequence stop: 447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled germ cell tumors"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 18; DB 1; I
100.0%; Pred. No. 2.5e+02;
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21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BM857244
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Matches 18; Conserv
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BM857244/c
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                       /lab host="Toplop""
/lab host="Toplop""
/clone lib="S20T665307"
/clone lib="S20T665307"
/note="Organ: Stomedth, Vector: pCNS, Site_l: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped incact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The CDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of EcoNI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 482)
NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LiCM263 row: b column: 07
High quality sequence start: 4
High quality sequence stop: 479.
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/dlone="IMAGE:3609126"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                           db_xref="taxon:9606"
clone="$20T665307-3-B02"
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                                            organism="Homo sapiens"
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  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 CTTTCGGCTCTCGGCTGC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTTTCGGCTCTCGGCTGC 18
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BE378810/c
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ORGANISM
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TITLE
JOURNAL
COMMENT
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/ Lissue type="Stomach"
/ Cell _ Type="Floating aggregates"
/ Cell _ Type="Tloating aggregates"
/ Cell _ Type="Tloating aggregates"
/ Cell _ Time="SNU-520"
/ Lab _ Dost="ToplOF"
/ Clone _ Lib="S21SNU520"
/ Lone _ Lib="Schadt"
/ Lone _ Lib="Schadt"
/ Lone _ Lib="Schadt"
/ Lone _ Lib="Schadted with Bap and then decapped with tabacco acid pyrophosphatase (RAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by tractmen of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about Gont. The CDNA vector was adjusted to a LNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. Coli ToplOF" by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: SeCR1; CDNB made by Oligo-dT prinning. Directionally closed into EccNI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ARP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 503)
1 (bases 1 to 503)
1 (bases 1, 504)
1, Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yusecong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; DB 2; Length 482; llarity 100.0%; Pred. No. 2.6e+02; Conservative 0; Mismatches 0; Indels
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21C Frontier Korean EST Project 2001
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High quality sequence stop: 503.
Location/Qualifiers
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Homo sapiens
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ORIGIN

0; Gaps Query Match
100.0%; Score 18; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels

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Search completed: February 5, 2005, 08:11:53 Job time : 2147.2 secs

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BT007208 Homo sapi
BT008248 Synthetic
AR054022 Sequence
AR172595 Sequence
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                                                                                                                                                          AR380913 Sequence
223116 H.sapiens b
AR044021 Sequence
AR124952 Sequence
AR124912 Sequence
AR144311 Sequence
BD243042 Antisense
CQ765842 Sequence
E58777 Screening m
I52011 Sequence
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BD097037 A BH4 fus
BD084108 Method of
BD102202 Method fo
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AR380885 Sequence
AX839772 Sequence
AX925686 Sequence
Z23115 H.sapiens b
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AR371662 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide inhibitors of bcl-xL
Patent: JP 2002519048-A 13 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
OS Artificial Sequence
PN JP 2002519048-A/13
PD 02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
PC ANTISENSE OLIGONUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-1999 JP 2000557839
02-JUL-1998 US 09/109614
CY A STEIN
BD097037
BD084108
BD102202
BT007208
BT008248
AR054022
                                                                                                                          152012
AR371662
AR380913
HSBCLKS
AR054021
AR118504
AR124952
AR124952
AR172594
AR172594
BD243042
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JP 2002519048-A/13.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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PN JP 2002519048-A/35
PD 02-JUL-2099
PP 02-JUL-1999 JP 2000557839
PR 02-JUL-1999 US 09/109614
PI CY A STEIN
PC C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/7125, PC
A61K47/42,
PC AASTENE DLIGONUCLEOTIDE
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FT misc binding (1) (1) (4)
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_Xref="taxon:32630"
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llarity 100.0%; Pred. No. 71;
Conservative 0; Mismatches 0
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Pred. No. 78;
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1 (Dases 1 to 87)
chou, Q., Maa, J. and Chang, C.
Self-primed amplification system
Patent: US 6207424-A 1 27-MAR-2001;
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/mol_type="unassigned DNA"
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Sequence 1 from patent US 6207424.
AR140001
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misc_binding (10)..(12)
misc_binding (15)..(18).
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Patent: JP 2002519048-A 35 02-JUL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
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Patent: JP 2002519048-A 34 02-ULL-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
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Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
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Oligonucleotide inhibitors of bcl-xL.
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02-JUL-2002
02-JUL-1999 JP 2000557839
02-JUL-1998 US 09/109614
CY A STEIN
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JP 2002519048-A/35.
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JP 2002519048-A/34.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                     /organism="Homo sapiens"
//mol type="unassigned DNA"
//db Xref="taxon:9606"
//note="MAP TO AL:17381.9-EXPRESSED IN PLACENTA, SIGNAL = 1.5-SWISSPROT HIT: 007817, EVALUE 2.00e-18-EST HUMAN HIT: 1.00e-65-NT HIT: 223115.1, EVALUE 1.00e-65"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                           Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
Human genome-defitved single exon nucleic acid probes useful for
analysis of gene expression in human placenta
Patent: WO 0157272-A 21529 09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 21565 09-AUG-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/db_xref="taxon:9606"
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Pred. No.
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CQ185285.1 GI:41180300
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/db_xref="taxon:5606"
/ncfe="wap TO ALILI381.9-EXPRESSED IN HEART, SIGNAL = 1.6-SWHSSPROT HIT: Q07817, EVALUE 2.00e-18-EST HUMAN HIT: 1.00e-65"
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/db xref="taxon:9606"
/db xref="taxon:9606"
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= 1.9-SWISSPROT HIT: 007817, EVALUE 2.00e-18-EST HUMAN
HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
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HUMAN GENOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVERCRI30> PB 0004 WO
33150-US 60/180, 312-151> 04 February 2000 (04.02.00)
60/207, 456-151> 26 May 2000 (26.05.00)
700-150- US 60/150> 26 May 2000 (26.05.00)
700-150- US 60/235, 359-511> 27 September 2000
700-150- US 60/234, 587-511> 21 September 2000
700-150- US 60/234, 687-511> 21 September 2000
700-150- US 60/234, 408-151> 30 June 2000 (30.06.00)
700-170>
Molecular Dynamics Sequence Listing Engine
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                       Human genome-derived single exon nucleic acid probes useful analysis of gene expression in human heart
Patent: WO 0157274-A 16681 09-AUG-2001;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
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Aeomica, Inc. (US)
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100.0%; Pred. No. 80;
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CQ234920.1 GI:41218197⊂
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PAT 23-JAN-2004

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Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                  Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
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/note="MAP TO AL117381.9~EXPRESSED IN BRAIN, SIGNAL =
2~SWISSPROT HIT: Q07817, EVALUE 2.00e-18~EST HUMAN HIT:
47820481.1, EVALUE 1.00e-65~NT HIT: Z23115.1, EVALUE
                                                                                                                                                                                                                                             Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human brain
Patent: WO 0157275-A 20846 09-AUG-2001;
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ive 0; Mismatches 0
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PE Corporation (NY) (US)
Location/Qualifiers
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CQ732731
                                          CQ346752 127 bp DNA
Sequence 20846 from Patent WO0157275.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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HIT: AW820481.1, EVALUE 1.00e-65-NT HIT: Z23115.1, EVALUE
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1.00e-65"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
Patent: WO 0186003-A 21250 15-NOV-2001;
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                     CQ272476 127 bp DNA
Sequence 20737 from Patent WO0157277.
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Sequence 21250 from Patent WO0186003.
CQ310145.
CQ310145.1 GI:41270722
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Length 127;

PAT 03-FEB-2004

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Length 387;

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Job time: 432.664 secs
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
Patent: WO 0157276-A 8597 09-AUG-2001;
Aeomica, Inc. (US)
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human placenta
Patent: WO 0157272-A 8448 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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CQ175406
CQ099589 587 bp Di
Seguence 8448 from Patent WO0157272.
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CQ138575
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0157274-A 6802 09-AUG-2001;
                                                                                                                                                                                                                                                                                                                        Aeomica, Inc. (US)
Location/Qualifiers
         GI:41170145
                                                            Homo sapiens (human)
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4, 2005, 15:50:53; Search time 232.23 Seconds (without alignments) 406.880 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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                                                                                                       February
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	OI .	AAZ46983	AAH19915	ABA72432	AAI52843	ABA38215	AAK47008	AAK20855	ABS46769	ABS21259	2 ACH84269	0 ACD94503	0 ADK66037	ACH46093	ABA59891	AAI39762	ABA28336	AAK34040	AAK08161	ABS33839	ABS08825	2 ACH70569
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* Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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AAH48169 AAH43464 AAH43464 AAM681699 ABZ83507 ABZ83507 AAM281638 AAT40079 AAM293614 AAM293614 AAM5966 AAM596169 AAM526104 AAM54187 AAM54187 AAM54187 AAM54187 AAM54187 AAM54187	AAS 0024 / ADG89403 ADN04260 ADO19866 AAX33182
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2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2386 2386 2386 2575 7372
	100000
000000000000000000000000000000000000000	98888
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 4 4 4 4 4 1 6 6 4 6

ALIGNMENTS

AAZ46983 standard; DNA; 18 BP.

RESULT 1

Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate; lung; bladder; bcl-2; vascular lesion; antisense; ss. Bcl-X1 mRNA specific antisense oligo M. (UYCO) UNIV COLUMBIA NEW YORK. 98US-00109614. 99WO-US015250. 14-APR-2000 (first entry) WPI; 2000-137140/12. WO200001393-A2. 02-JUL-1999; Homo sapiens. 02-JUL-1998; 13-JAN-2000. AAZ46983; Stein CA;

New antisense oligonucleotides inhibiting the anti-apoptotic protein.bcl-xL, useful for reducing bcl-xL production in tumor cells to treat cancer or in vascular cells to promote the regression of vascular lesions.

Claim 1; Fig 1; 69pp; English.

which reduce or eliminate expression of the anti-apoptotic protein bol-which reduce or eliminate expression of the anti-apoptotic protein bol-xi. The oligomorleotides can be introduced into tumour cells to reduce bol-xi production to treat cancer, especially epithelial cancer, e.g. prostate, lung or bladder cancer. Oligomorleotides comprising one or more bases with a C-5 propynyl pyrimidine modification may especially be used to reduce levels of bol-2 family proteins (to which bol-xi belongs) in such treatment. The oligomorleotides can be introduced into vascular cells to reduce bol-xi production to promote the regression of vascular The invention provides antisense oligonucleotides or their derivatives

us-09-753-169a-13.rng

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ABA72432 standard; DNA; 127
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                                                                                                  ABA72432;
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       RESULT 3
                              ABA72432
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lesions. They can also be included with a carrier (and optionally tetra meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in pharmaceutical compositions, useful as above. Sequences AAZ46971-983 represent antisense oligos specific for the bcl-Xl mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a self-priming nucleic acid polymerase (SNAP) primer (1) for copying a target nucleic acid (TNA) comprising, from 3-5, a sense, target-specific binding domain (TBD), a non-target, antisense primer binding domain (PBD), non-target, sense PBD and an antisense TBD. SNAP primers are useful for copying a target nucleic acid or a mixture of at least two different target nucleic acids. Methods comprising SNAPs are less likely to produce variable and erroneous signals in multiplex assays. The present sequence represents a specifically claimed single SNAP primer designated SPAS-BCL-1001, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Self-priming nucleic acid polymerase; SNAP; primer; amplification; BCL; bcl-xL; human; ss.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single SNAP primer SPAS-BCL-1001 directed toward bcl-xS and bcl-xL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New self-priming nucleic acid polymerase primer for copying target
nucleic acid, contains (anti) sense target specific and non-target
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                                                                                                                                                                 / Match 100.0%; Score 18; DB 3; Length 18; Local Similarity 100.0%; Pred. No. 13; Length 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                         Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specifically claimed single SNAP prints a directed toward bcl-xS and bcl-xL
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nes 18; Conservative (
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AAH19

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human forcal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                          Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                            Human foetal liver single exon nucleic acid probe #20737
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100.0%; Pred. No. 16;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
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(first entry)
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52.
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                                                                                                                                                                                        WO200157277-A2
                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
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Gaps

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0; Indels

Mismatches

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1 AACCAGCGGTTGAAGCGT 18

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87

70 AACCAGCGGTTGAAGCGT

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 16;
; Mismatches 0; Indels
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                                                                                                                                                           Claim 4; SEQ ID NO 16681; 530pp; English.
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                                  Chen W, Rank DR;
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(MOLE-) MOLECULAR DYNAMICS INC.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0032466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023599P.
04-OCT-2000; 2000GB-00024263.
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Best Local Similarity 100.
Matches 18; Conservative
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                                  Hanzel DK,
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                                  Penn SG,
                                                                                                                            hearts.
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                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene expression; heart; microarray; vascular system; probe;
cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 21529; 654pp; English.
                                                                                                                                                                                                                                                                                                           Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                    gene expression in human placenta.
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2000US-0234687P.
2000US-0236359P.
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2000US-00608408.
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2000US-00632366
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2000US-0236359P
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                                                                                     30-JAN-2001; 2001WO-US000663
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Matches 18; Conservative
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                 WO200157272-A2
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27-SEP-2000;
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03-AUG-2000;
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51 AACCAGCGGTTGAAGCGT

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 4; Length 127; 100.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                     Sequence 127 BP; 28 A; 40 C; 33 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AACCAGCGGTTGAAGCGT 18
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30-JUN-2000; 2000US-00608408.
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27-SEP-2000; 2000US-0236359P.
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hes 18; Conserv
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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                                                                                                                                                                Human, single exon nucleic acid probe; liver, cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
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16;
                                                                                                                                Human liver single exon probe, SEQ ID No 21759.
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Pred. No. 1
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                 ABS46769 standard; DNA; 127
                                                                                                                                                                                                    coronary heart disease; ss
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                 25-FEB-2003
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RESULT 8
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Gaps

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100.0%; Score 18; DB 4; Length 127; 100.0%; Pred. No. 16; 0; Indels cive 0; Mismatches 0; Indels

Local Similarity 100 nes 18; Conservative

Query Match Best Loc Matches

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, comprising ene expression in a sample of acid expressed in the human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (a) and probe is included in the above mentioned microarray; ascidited exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, having a fragment identical to the predicted exon; the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human
                                                                                                                                                                                                                                                                                                    Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                       genome-derived single exon probe ORF from lung SEQ ID No 21250.
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                                                                                                                                                                                                                                     chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                   single exon probe; asthma; lung cancer; COPD; ILD;
                                                                                                                                                                                                                                                                                                                                                                                                hyaline membrane disease; open reading frame; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 measure gene expression in human lung samples.
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                                         ABS21259 standard; DNA; 127 BP.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408,
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                                                                                                                            (first entry)
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RESULT 9
ABS21259
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cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoldosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence data for this patent disease. The invention is a single exon probe open reading frame of the thromation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human probes cited above, where each of the plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human genome-derived single exon nucleic acid probes useful for hum: gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; probe; as; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
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derived mRNA and for the study of lung diseases such as
                                                                                                                                                                                                                                                                                                          6; Length 127;
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                        100.0%;
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Best Local Similarity
Matches 18; Conserv
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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us-09-753-169a-13.rng

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measuring human gene expression, a wector comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above mentioned amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (ach record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising calterations in the genomic locus that includes their exon, in assessing alterations in the genomic locus that includes their exon, in assessing calterations in the genomic locus that includes their exon, in assessing or in expressing the ORF-encoded peptide. The sequence data for this single exon probe of the inventon. Note: The sequence data for this in electronic formal directly from the print of the printed specification, but was obtained in the language.
      exon microarray for measuring human gene expression, a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              segdata.uspto.gov/sequence.html?DocID=20030194704
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Sequence 179 BP; 37 A; 53 C; 48 G; 41 T; 0 U; 0 Other;

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Gaps
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  DB 12; Length 179;
                              0; Indels
100.0%; Score 18; DB
100.0%; Pred. No. 17;
ive 0; Mismatches
                            18; Conservative
                 Best Local Similarity
  Query Match
                              Matches
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97 AACCAGCGGTTGAAGCGT 셤

Human colon cancer cell expressed cDNA #2915. ACD94503 standard; cDNA; 299 BP (first entry) 23-SEP-2003 ACD94503; ACD94503,

Open reading frame detection; genome sequencing; colon cancer; breast cancer; population genome analysis; genetic shift; cancer; antibictic resistance; antibictic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; gene; sa

Homo sapiens.

US2002155438-A1.

24-OCT-2002.

99US-00406117. 27-SEP-1999; 98US-00196716. 20-NOV-1998;

(SIMP/) SIMPSON A J G. (BREN/) BRENTANI R R. NETO E D

Brentani RR; Neto ED, Simpson AJG,

WPI; 2003-182626/18.

Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at

The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonoucleotide primer (1) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (1), amplifying cond amplifying steps with different primers and sequencing, preparing and amplifying steps with different primers and sequencing, resulting nucleic acids. The method is useful for: determining that a known conclectide sequence from a genome of an organism corresponds to a nucleic acid molecule from a genome of an organism; and for sequencing nucleic acid molecule from a genome of an organism; and for sequencing all or part of a genome of an organism. mRNA is obtained from mammalian or human cell which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of oppulations of subjects and can be used to carry out genetic analyses of populations of subjects and can be used to study living a systems to determine if, e.g. there have been genetic shifts which render an individual or population more or less likely to be afflicted with diseases such as cancer, to determine antibiotic resistance or non-tile congnitual diseases, and the risk of affliction to a foetus, as well as the study of whether the conditions are likely to be passed to offerping. through ova or sperm. The analyses for pathological conditions can be carried out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be studied to determine if resistance genes represent, defects in plant genomes can also be studied in this way. Similarly, the method permits determination of the pathogens which integrate into the genome, such as retroviruses and other integrating viruses such as influenza virus, have undergone shifts or mutations, which may require different approaches therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially trypanosomes, different types of Plasmodium, etc. The method essentially eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library low stringency for preparing single-stranded cDNA from mRNA of Example 9; Page 432; 959pp; English individua

Sequence 299 BP; 64 A; 95 C; 74 G; 66 T; 0 U; 0 Other;

Gaps ; Score 18; DB 10; Length 299; Pred. No. 18; 0; Indels Mismatches 100.0%; Score 18; ; 0 100.08; 18; Conservative Query Match Best Local Similarity Matches

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1 AACCAGCGGTTGAAGCGT 18 75 AACCAGCGGTTGAAGCGT

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ADK66037,

ADK66037 standard; DNA; 337 BP

ADK66037;

06-MAY-2004 (first entry)

Standardized polynucleotide system polynucleotide #8.

ss; standardized polynucleotide system; medical diagnosis; functional genomics; sample analysis; pharmacogenomics; sample analysis.

Unidentified.

DE10209071-A1.

25-SEP-2003.

28-FEB-2002; 2002DE-01009071.

28-FEB-2002; 2002DE-01009071.

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SEQ ID NO 33305; 44pp; English.
   antisense DNA or RNA.
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Matches 18; Conserv
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                                                                                                                                    The present invention relates to a standardized polynucleotide system, which comprises at least one carrier nucleic acid, at least 3 oligonucleotides, as primers and target-specific, fluorescently labeled probe and optionally at least one set of stabilized controls (standard RNA or DNA) of known concentration and instructions. The system comprises any of 20 sets of one control, two primers and one target-specific probe. The standardized polynucleotide system can be used for quantitative, real-time detection of target nucleic acids, especially analysis of genes or gene products, e.g. for individualized medical diagnosis, in veterinary medicine, functional genomics, clinical pharmacology, pharmacogenetics, pharmaccutical testing, analysis of food or environmental samples and also for ultra-sensitive detection of proteins by immuno-PCR. The present sequence is a polynucleotide used in the system of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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                                                                   Standardized polynucleotide system, useful for quantitative, real-time determination of nucleic acid, comprises stabilized standards, primers
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                                                                                                                                                                                                                                                                                                       Sequence 337 BP; 71 A; 91 C; 101 G; 74 T; 0 U; 0 Other;
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(ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACH46093 standard; cDNA; 492 BP
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                                                                                                                Claim 1; Page 7; 38pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human infant brain cDNA #156.
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STACHE-CRAIN E
DICKSON M C.
JONES L W.
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                                           WPI; 2003-732912/70
                        Rost A;
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tes 18; Conserv
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                     Koehler T,
                                                                                          and probe.
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(STAC/)
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisonse BNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/RST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. html?DocID=20030073623
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
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2000US-0207456P.
2000US-00608408.
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human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 18; DB 4; Length 587; 100.0%; Pred. No. 19;
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genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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26-MAY-2000; 2000US-0270456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0234587P.

04-OCT-2000; 2000US-0234587P.
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1es 18; Conservative
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Query Match 100.0%; Score 18; DB 4; Length 587; Best Local Similarity 100.0%; Pred. No. 19; Matches 18; Conservative 0; Mismatches 0; Indels

1 AACCAGCGGTTGAAGCGT 18

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Db 450 AACCAGCGTTGAAGCGT 467
Search completed: February 4, 2005, 21:52:4
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Search completed: February 4, 2005, 21:52:44 Job time: 232.23 secs

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BF929309 IL2-NT020
BF886802 PM2-CI011
BF804861 PW2-CI011
AI904167 CM-BT043-
BF82358 RC5-RT005
AW820481 QV2-ST029
BE925384 PW0-AN008
AW820330 QV2-ST029
BM348649 K-EST0085
BM348649 K-EST0085
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W01420 za73d06.rl
                                                                                            February 4, 2005, 20:41:45; Search time 2146.2 Seconds (without alignments) 305.616 Million cell updates/sec
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BM818387 K-EST008
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                                                                                                                                                                                                                                                                                                                              65645750
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                       32822875 seqs, 18219865908 residues
                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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BI051278
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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Busukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Bmall: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL3-CT0215-170
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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/mol type="maxna" | //mol type="maxna" | //mol type="maxna" | //mol type="maxna" | //mol type="maxna" | //mole="taxon:9606" | //dev stage="Adult" | //dev stage="Adult" | //dev stage="maxna" | //mole="Organ: nervous tumor; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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QV3-ET0175-011200-514-a04 ET0175 Homo sapiens CDNA, mRNA sequence.
BF880488
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IL2-NT0202-081200-298-D05 NT0202 Homo sapiens cDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br

This asquence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-NT0202-

081200-298-D05&t2=2000-12-08&t4=1)

Seq primer: puc 18 forward

High quality sequence stops: 167.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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100.0%; Score 18; DB 2; Length 154; 100.0%; Pred. No. 49; or Indels ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 18; Conservative

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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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/mol_type="mRNA"
/db_rref="taxon:9606"
/dev_stage="Adult"
/clone_lib="Er0175"
/note="forgan: lung tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 194)

1 bases I to 194)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Go'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0175-011200-514-a04&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence stor: 17
High quality sequence stop: 194.
Location/Qualifiers
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1 (bases 1 to 216)

1 bias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
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                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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PM2-CI0111-091100-004-b10 CI0111 Homo sapiens CDNA,
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  GI:12270718
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                                           sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
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VERSION
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                                                                                                                                             AUTHORS
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SOURCE
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BF806802
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//db_xref="taxon:9606"
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//clone_lib="CI0111"
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Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
Site_5: SmaI; A mini-library was made by cloning products
Site_5: SmaI; A mini-library was made by cloning products
Site_5: SmaI; A mini-library was made by cloning products
No. 196,716 - Ludwig Institute for Cancer Research
Drofiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 213)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Glanstein, A., deoliveira, P.S., Matsukuma, A., Baia, G.S., Simpson, D.H., O'Hare, M.J., Soares, F., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001

Email: asimpsonoludwig org.br
This asimpsonoludwig org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=PM2&t2=PM2-CI0111-
091100-004-bl0&t3=2000-11-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence start: 25
Location/Qualifiers
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mRNA sequence.
                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shorgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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PM2-CI0111-041100-001-d01 CI0111 Homo sapiens cDNA,
BF804861
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Gaps

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 28). Dias Neto. E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carraho, A.F., Mateukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                          /dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP823588 221200-011-G02 RT0055 Homo sapiens CDNA, mRNA sequence.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0055-21200-011-G02&t5=2000-11-2-22&t4=1)
Seq primer: puc 18 forward
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/clone lib="RT0055"
/note="Organ: Right tumor; Vector: puc18; Site_1: Sma1;
/note="Organ: A mini-library was made by cloning products
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 1; Length 233; 100.0%; Pred. No. 52; ive 0; Mismatches 0; Indels
                                                                                 organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                           /mol_type="mRNA"
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Seq primer: puc 18 forward.
Location/Qualifiers
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75 AACCAGCGGTTGAAGCGT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF823588.1 GI:12164528
                                                                                                                                                                   'sex="female"
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/clone lib="Cloll"

/note="Organ: colon ins; Vector: puc18; Site_1: Sma1;

Site_2: Sma1, A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under
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1 (bases 1 to 2 arcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT043-089.html
&t3=09029&t4=1)
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                                                                                                           Eax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-CI0111-041100-001-d01&t3=2000-11-04&t4=1)
Seq primer: puc 18 forward High quality sequence start: 13 High quality sequence start: 13 High quality sequence stop: 232.
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                             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; DB 2; Length 232; 100.0%; Pred. No. 52;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
  Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 100...
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                                                                                 Tel: +55-11-2704922
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Pred. No. 54;
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/organism="Homo sapiens"
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High quality sequence start: 16
High quality sequence stop: 339
Location/Qualifiers
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0087"
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    1 AACCAGCGGTTGAAGCGT 18
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100.0%;
                                     242 AACCAGCGGTTGAAGCGT
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Fax: +55-11-2707001
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AW820530/c
                                                                                                                            BE925384/c
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1 (bases 1 to 312)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Soldan, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Harre, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Adult"
/clone lib="ST0298"
/note="Organ: stomach; Vector: puc18; Site 1: Smal;
Site_2: Smal; A minl-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Final: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-140 200-042-fl2&t3=2000-02-14&t4=1)
                                                                                                                                                                                                                                                                                                                                                                             AW820481 532 bp mRNA linear EST 17-MAY-2000 QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                  Length 283;
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                                                                                                                                                                                          0; Indels
                                                                                                                                                100.0%; Score 18; DB 2; 100.0%; Pred. No. 53;
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100.0%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches
                                                                                   low stringency conditions."
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High quality sequence Btop: 332.
Location/Qualifiers
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/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity
Matches 18; Conserv
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AW820530 358 bp mRNA linear EST 17-MAY-2000 QV2-ST0298-220200-061-d10 ST0298 Homo sapiens cDNA, mRNA sequence. AW820530
               EST 02-OCT-2000
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This enquence we seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=PMO-AN0087-180 800-001-b07&t3=2000-08-18&t4=1)
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                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 339)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
339 bp mRNA linear
PMO-AN0087-180800-001-b07 AN0087 Homo sapiens CDNA,
BE925384
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/clone_lib="$20T665307"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intext mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
ECORI which site is also included in vector. An RNA strand
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1 (Dases 1 to 418)

1 (Dases 2 to 418)

1 (Dases 3 to 418)

1 (Dases 3 to 418)

1 (Dases 4 to 418)

1 (Dases 6 to 418)

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CM3-GN0297-110101-607-£03 GN0297 Homo sapiens CDNA, mRNA sequence.
BIO51278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ropolof' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                        Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S2 Boeun-Gong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongewingemail.kribb.re.kr
Plant: 4 row: F column: 03
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                    EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-4-F03"
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High quality sequence stop: 396.
Location/Qualifiers
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Kim,Y.S.
21C Frontier Korean E.
Unpublished (2002)
Contact: Kim YS
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Best Local Similarity 100.
Matches 18; Conservative
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/clone_lib="ST0298"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3 arcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-ST0298-220
200-061-dl0&t3=2000-02-22&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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High quality sequence start: 44
High quality sequence stop: 358.
Location/Qualifiers
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                                                                         Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4.18)
1 (bases 1 to 4.18)
2, Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                             Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This unry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0297-
110101-607-f03&t3=2001-01-11&t4=1)
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K-EST0014589 S6SNU620 Homo sapiens CDNA clone S6SNU620-4-C01 5',
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                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/clone_lib="GN0297"
/note="Organ: placenta_normal; Vector: puc18; Site_1:
Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the DUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 18; DB 4; Length 418; 100.0%; Pred. No. 55;
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                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 4 row: C column: 01
High quality sequence stop: 418.
Location/Qualifiers
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sex="F"
                                                                                                                                                                                                       Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 418
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +82-42-860-4409
                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Kim YS
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                                                                                                                                                                                                                                                                                          1. .418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .418
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Best Local Similarity
Matches 18; Conserv
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BM741875/c
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                      FEATURES
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// Actore="Organ: Stoomed; Vector: pCNS; Site 1: ECCRI; Site 2: Not1; The poly (A) + RNA was dephosphorylated with baterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof; by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W01420 arNu linear EST 18-APR-1996 za73d06.rl Soares fetal_lung_NbHL19W Homo sapiens cDNA clone INAGE:298187 5' sīmilar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X.;, mRNA sequence.
W01420 GI:1273428
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( Dases I to 437)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: mob.REGA+ET High quality sequence stop: 383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Soares fetal lung NbHL19W"
/note="organ: lung; Vector: pT713D (Pharmacia) with a
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Length 418;
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NbH119W"
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ilarity 100.0%; Pred. No. 55;
Conservative 0; Mismatches
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mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:298187"
cell line- ..../lab host="Top10F'"
/rlone lib="S6SNU620"
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Fax: 314 286 1810
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ORIGIN

Gaps 0; Query Match 100.0%; Score 18; DB 7; Length 437; Best Local Similarity 100.0%; Pred. No. 55; Matches 18; Conservative 0; Mismatches 0; Indels

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1 AACCAGCGGTTGAAGCGT 18

403 AACCAGCGGTTGAAGCGT 386

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Search completed: February 5, 2005, 08:11:53 Job time : 2146.2 secs